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Result
No.
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Listing first 45 summaries
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Aaximum DB seq length: 2000000000
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1 MDTMMLNVRNLFEQLVRRVE.....SKSATNLGRQGNEFASPMLK 632
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/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
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/cgn2_6/ptcdata/1/paa/US087_COMB.pep:*
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                                                                                                                                                              Description
Sequence 1796, Ap
Sequence 2, Appli
Sequence 585, App
Sequence 3192, Ap
Sequence 72082, A
Sequence 413, App
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Sequence 598, App	-60-389-987-5	2022	10.3	334	5
901,	US-60-146-315-9	367	14.2	460	44
150251	us-09-791-537-150	385	14.7	477	43
4551,	US-60-191-637-4551	384	14.7	477	42
10	US-60-167-217-463	384	14.7	477	41
65301,	US-09-791-537-653	384	14.7	477	40
equence 4533, A	US-09-614-150-4533	384	14.7	477	39
7733	US-09-791-537-7733	383	14.7	477	38
equence 3586	US-09-791-537-358	383	14.7	477	37
3547	US-60-162-245-354	114	16.1	521	36
. 6, A	US-09-881-736-6	681	•	4	35
equence 7625	US-09-791-537	189		547.5	34
6453,	us-60-169-868	135		549	ü
е 3866,	US-60-162-245	135		549	32
č	US-09-488-725	119	17.9	581	3
equence 44317,	PCT-US01-08631	1139	٠	618	30
50263,	PCT-US01-08631	1086	٠	618	29
•	PCT-US01-08631	665		618	28
45146,	PCT-US01-08631	4318		625	27
e 2570,	US-60-311-261	872	٠	631	26
	PCT-US01-08656	872	٠	631	25
e 696,	US-60-186-655	142		632	24
294,	US-60-207-215	187	٠	646	23
968,	US-60-186-662	148			22
967,	US-60-186-662	165		749.5	21
Sequence 30526, A	SD	625	26.6	864	20
4912	US-09-791-537	625		864	19
3096	US-09-614-150	625.		864	18
Sequence 1025, Ap	US-60-182-569	191		889.5	17
1026	US-60-182-569	201		940.5	16
9072,	PCT-US01-08656	256		971.5	15
equence 6751	US-10-235-926	243		1103.5	14
e 6751,	US-09-758-472	243	34.0	1103.5	13
e 1045,	US-60-412-418	255	36.4	1182	12
e 1045,	US-60-389-987	255	36.4	1182	11
e 1458	US-09-629-4691	255		1182	10
4, Appl	9-881-736-4	628	84.3	2734	9
equence 36304,	US-09-791-537-	628	4.	2734	8
	US-09-833-790-42	570	0	2919	7
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### ALIGNMENTS

RESULT 1 US-09-791-537-1796

Sequence 1796, Application US/09791537 GENERAL INFORMATION:

X

QY 1 MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK 60	Query Match 100.0%; Score 3243; DB 21; Length 632; Best Local Similarity 100.0%; Pred. No.>2.8e-263; Matches 632; Conservative 0; Mismatches 0; Indels 0;	; LENOTH: 632 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-791-537-1796	CURRENT APPLICATION NUMBER: US/99/191,53/ CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 153055 SOFTWARE: PatentIn version 3.0 SEQ ID NO 1796	APPLICANT: Danzer, Joseph TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210	APPLICANT: Bionomix, Inc.
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)LLMK 60 )LLMK 60 )LSEE 120	aps 0;			S AND FAMIL	
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Sequence 2, Application US/09881736

GENERAL INFORMATION:
APPLICANT: Glotzer, Michael
APPLICANT: Jantsch-Plunger, Verena
APPLICANT: Jantsch-Plunger, Verena
APPLICANT: Mishina, Masanori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyk 4 polypeptides, DNA molecules encoding them and their use in
TITLE OF INVENTION: Screening methods
FILE REFERENCE: 0652.226001/EKS/AES
CURRENT APPLICATION NUMBER: US/09/881,736
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR FILING DATE: 2000-104-30
PRIOR FILING DATE: 2000-104-30
PRIOR APPLICATION NUMBER: EP 01 110 554.1
PRIOR APPLICATION NUMBER: 60/241,231
PRIOR APPLICATION NUMBER: 60/241,231
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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                100.0%;
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  Score 3243; DB 22;
Pred. No. 2.8e-263;
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                                                                       ; TYPE: PRT
; ORGANISM: Homo
US-09-641-377-585
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APPLICANT: GASSENHUBER, JOHANN
APPLICANT: TAMPE, JENS
TITLE OF INVENTION: HUWAN DNA SEQUENCES
FILE REFERENCE: 087100/0106
CURRENT APPLICATION NUMBER: US/09/641,377
CURRENT FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/149,499
PRIOR FILING DATE: 1999-08-18
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PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 1793
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 585
LENGTH: 632
                Query Match
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                Score 3237; DB 20;
Pred. No. 8.9e-263;
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FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT EILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-05-20
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                               PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR PELICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
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APPLICANT: Hyseg Inc
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     SEQ
   SOFTWARE:
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; TYPE: PRT
; ORGANISM: Homo :
US-09-791-537-72082
                                                                                                                                                                                                                                    RESULT 5
US-09-791-537-72082
; Sequence 72082, Application
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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                                               CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 72082
LENGTH: 632
                                                                                                                             APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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Pred. No. 1.9e-262;
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RESULT 6
US-09-833-790-413
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; ORGANISM: Homo sapiens US-09-833-790-413
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Best Local Similarity
Matches 630; Conserv
                                                    SEQ ID NO 413
                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CATELLE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Wang,
APPLICANT: Secris
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                           TYPE: PF
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Secrist, Heather
Mohamath, Raodoh
Indirias, Carol Y.
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Pred. No. 3.5e-262;
0; Mismatches 2;
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US-09-833-790-427

Sequence 427, Application US/09
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
US-09-833-790-427
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                                  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 427
LENGTH: 570
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Best Local
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                                                                                    FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
          LENGTH: 57
TYPE: PRT
ORGANISM:
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Secrist, Heather
Mohamath, Raodoh
Indirias, Carol Y.
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                                                              Version
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APPLICANT: DANZEY, JOSEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 36304
LENGTH: 628
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-36304
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Matches 534
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                                                                                                         Local Similarity
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                                             MDTMMLNVRNLFEQLVRRVEILSEGNE-VQFIQLAKDFEDFRKKWQRTDHELGKYKDLLM
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                               MDTTMVNLWTLFEQLVRRMEIINEGNESIEFIQVVKDFEDFRKKYQRTNQELEKFKDLLL
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84.4%; Pred. No. 2e-220;
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Query Match
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Matches 534; Conserv
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                                                                                                                      SEQ ID NO 4
                                                                                                                                                                                                                      APPLICANT: Glotzer, Michael
APPLICANT: Jantsch-Plunger, Verena
APPLICANT: Romano, Alper
APPLICANT: Romano, Alper
APPLICANT: Mishima, Massnori
APPLICANT: Mishima, Massnori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Screening methods
TITLE OF INVENTION: Screening methods
FILE REFERENCE: 0652.2260001/EKS/AES
CURRENT APPLICATION NUMBER: US/09/881,736
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR APPLICATION NUMBER: EP 01 110 554.1
PRIOR FILING DATE: 2001-04-30
DENIOR FILING DATE: 2001-04-30
DENIOR FILING DATE: 2001-04-30
DENIOR FILING DATE: 2001-04-30
DENIOR FILING DATE: 2001-04-30
                                                                                                                                  PRIOR APPLICATION NUMBER: To be
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
                                                                                       LENGTH: 62
TYPE: PRT
                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/241,231 PRIOR FILING DATE: 2000-10-18
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84.3%; Score 2734; DB 2 ilarity 84.4%; Pred. No. 2e-220; Conservative 47; Mismatches 4
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APPLICANT: ONSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUI
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
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SUGIYAMA, TOMOYASU
WAKAMATSU, AI
NAGAI, KEIICHI
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N-LSKSTPREGNKSKSATNLGQQGKEFPAPYLK
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ISHII, SHIZUKO
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KEKFLRVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIA 456

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PRIOR APPLICATION NUMBER: 60/183,322
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14587
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-629-469a-14587
                                                            ; ORGANISM: Homo sapiens US-60-389-987-1045
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                                                                                        CURRENT APPLICATION UNLER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
RUMBER OF SEO ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1045
LENGTH: 255
TYPE: PRT
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GENERAL INFORMATION:
              Query Match
Best Local
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Best Local :
 Matches
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROFILE REFERENCE: 660088.465P2
                                                                                                                                                                                                                                                                                                              APPLICANT: Ghosh,
APPLICANT: Fahy,
APPLICANT: Zhang,
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Gibson, Bradford W
Taylor, Steven W.
Glenn, Gary M.
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Score 1182; DB 27;
Pred. No. 2.3e-90;
0; Mismatches 2;
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Pred. No. 2.3e-90;
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US-60-412-418-1045
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TOENTIFIED IN THE MITOCHONDRIAL PROT
FILE REFERENCE: 660088.465P3
CURRENT APPLICATION NUMBER: US/60/412,418
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1045
LENGTH: 255
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Sequence 6751, Appli
GENERAL INFORMATION:
                                                                          NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver.
SEQ ID NO 6751
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Best Local Similarity
Matches 234; Conser
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                                                                                                                           PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/758,472
CURRENT FILING DATE: 2001-01-11
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
                                                                                                                                                            PRIOR FILING DATE: 2000-01-31
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PHOO1
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                                               TYPE: PRT
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                            ORGANISM: Homo sapiens
NAME/KEY: SITE
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Pred. No. 2
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OTHER INFORMATION: 3
NAME/KEY: SITE
LOCATION: (242)
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OTHER INFORMATION: Xaa equals any of the naturally
                                                                                                          NAME/KEY: misc_feature LOCATION: (240)
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124 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR
                                                                                                                                                                                                                       h 34.0%;
Similarity 97.4%;
                                                                                                                                                       EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVEKLQ-CCPNDGG
             EKRRSTSRQFYDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGG
                                                                          QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR 180
                                                                                                      AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE
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SOFTWARE: PatentIn Ver. SEQ ID NO 6751 Sequence 6751, Application US/10235926 GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04 PRIOR FILING DATE: 2000-02-04 NUMBER OF SEQ ID NOS: 9632 PRIOR APPLICATION NUMBER: 09/758,472 PRIOR FILING DATE: 2001-01-11 CURRENT APPLICATION NUMBER: US/10/235,926
CURRENT FILING DATE: 2002-09-06 TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PH001ClN APPLICANT: Rosen et al. TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: misc\_feature 2002-09-0 and Antibodies

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PCT-US01-08656-9072
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PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: CUSTOM
SEQ ID NO 9072
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                               T-US01-08656-9072
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                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 205; Conservat
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (7):.(33)
OTHER INFORMATION: PROTEIN GTPASE DOMAIN ACTIVATION domain identified by
OTHER INFORMATION: ematrix, accession number PD00930A, p-value-7.324e-15,
OTHER INFORMATION: 25.62
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                                 588 TPSS 591
                                                                181 LWEYWEFSFMDGWEQGGTFDPLHVIENSNAFSTPQTPDIKAVPGGGLCVHFTAGEAEIQK 240
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Pred. No: 1.2e-72;
3; Mismatches 27;
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Search completed: July Job time: 307 secs ω 2003, 10:02:52

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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### ALIGNMENTS

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A Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl
A Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
A Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
A Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner I.
A Membutt R., Korn B., Klein M., Poustka A.;
T "Towards a Catalog of Human Genes and Proteins: Sequencing and Towards a Catalog of Human Genes and Proteins: Sequencing and Towards as Il:42-435(2001).
T Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
Genome Res. 11:42-435(2001).
R EMBL; AL136794; CAB66728.1; -.
R HSSP; 207960; IRGP.
InterPro; IPRO
Pfam; PF00130;
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Q9H0H5;
Q1-MAR-2001
Q1-MAR-2001
Q1-JUN-2002
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                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
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     IPR002219; DAG_PE-bind
IPR000198; RhoGAP.
0130; DAG_PE-bind; 1.
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01-OCT-2000 (TrEMBLrel. 15
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01-UN-2002 fis, clone H
                                         Larvota; Metazoa; Chordata;

"arvota; Metazoa; Primates;
     Kawakami
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SMART; SM00109; C1; 1.
SMART; SM000324; RhoGAP; 1.
PROSITE; pS00479; DAG_PE_BIND_DOM_1;
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HSSP; Q07960; 1RGP.
InterPro; IPRO02219; DAG_PE-bind.
InterPro; IPRO00198; RhoGAP.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00109; C1; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00324; RhoGAP; I.
 Q9P250;
Q9P250;
Q1-CCT-2000 (
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KIAA1478 prot
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RT "Prediction of the coding sequences of unidentified human genes.XVII.The complete sequences of 100 new cDNA clones from which code for large proteins in vitro.";
L DNA Res. 7:143-150(2000).
R EMBL; AB040911; BAA96002.1;
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InterPro; IPR00198; RhoGAP.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00130; DAG_PE-bind; 1.
SMARR; SM00109; C1; 1.
SMARR; SM00109; C1; 1.
SMARR; SM00324; RhoGAP; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; UN PROSITE; PS00479; DAG_PE_BIND_DOM_2; 1.
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SEQUENCE 570 AA; 63468 MW; A03F36CC
   Q9BZ74
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Pred. No. 1.9e-191;
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01-JUN-2001
01-JUN-2001
01-DEC-2001
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam;
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Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
SEQUENCE 628 AA; 70013 MW;
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Q07960; 1RGP.
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                              MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
                                                                                                                                                                       AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE
                                                                                                                                                                                                                                                                                                                                                        MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK
        TLTKNTPRFGSKSKSATNLGRQGNFFASPMLK
                                                                                                                                                                                                                  YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
                                                                                                                                      MIPRIVVHCVNEIEQRGLTETGLYRILGCDSTVK-LKEKFLRVKTVPLVSKVDDIHAICS
                                                                                                                                                                                                                                           EKRCSSSRQFVDGPSGPVKETRSIGSTVDQGNESIVAKTTVTVPKDGGPIKAVPTIETVP
                                                                                                                                                                                                                                                   EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP
                                                                                                                                                                                                                                                                                                             AETERSALDYKLKHAHNQVDADIQRRRRAEANCEKLEQQIQLIGEMFLCDISGSIQLSGE
                                                                                                                                                                                                                                                                                                                                              MDTTMLNMRNLFEQLVRGAEILKEGNELQFIQLVKDFEDFFKKWERTDYELGKYKDLLIK
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87.0%;
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Pred. No. 6.1e
31; Mismatches
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel
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Submitted (JUL-2001) to the E
EMBL; AF079974; AADA0487.1; -
EMBL; AB030252; BAA90248.1; -
EMBL; AF212321; AAG43540.1; -
EMBL; AF212320; AAG43539.1; -
EMBL; BC010715; AAH10715.1; -
HSSP; 007960; 1RGP.
                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1349423; Racgap1.
InterPro; IPR002219; DAG_PE-b
InterPro; IPR00198; RhoGAP.
Pfam; PF00130; DAG_PE-bind; 1
Pfam; PF00620; RhoGAP; 1.
SMART; SM00109; C1; 1.
SMART; SM001344; RhoGAP; 1.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RAC GTPase-activating protein (GTPase activating protein (GTPase activating protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van de Putte T., Zwijsen A.,
Francis A., Baekelandt V., K
"Mice with a homozygous gene
during pre-implantation deve
Mech. Dev. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                             PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
PS50081; DAG_PE_BIND_DOM_2; 1.
628 AA; 70158 MW; 8D1B9DEC3CE057BE
MDTMMLNVRNLFEQLVRRVEILSEGNE-VQFIQLAKDFEDFRKKWQRTDHELGKYKDLLM
                                                                                                                                                                 MDTTMVNLWTLFEQLVRRMEI INEGNESIEFIQVVKDFEDFRKKYQRTNQELEKFKDLLL
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., Kitamura T.,
cDNA for GTPase a
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V., Kozak C.A., Zei
gene trap vector
n development.";
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No. 16
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Zerial
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Cerial M., H
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SUGATO S., Shiratori A., Sudo H.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Masuho Y.,
                                                                                                                                                                                      Yamamoto J., Wakamatsu A., Nakamura Ninomiya K., Iwayanagi T.; "NEDO human cDNA sequencing project. Submitted (AUG-2000) to the EMBL/Gen EMBL; AK022726; BAB14206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     Q9H9L9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ12664 fis, clone NT2RM4002226, weakly sim
                                                                                                                                                                             HSSP;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                            Pro; IPR001092; HLH_basic.
Pro; IPR000198; RhoGAP.
Pro; IPR000198; RhoGAP.
; 1.
; SM00324; RhoGAP; 1.
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                                                                                                                                                                            Q07960; 1RGP.
                                                                Similarity
SQFMMVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTPSSSSSLSQRVR:|||||:|||||||:|||
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                                                  36.4%;
ilarity 99.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                 Score 1182; D. Pred. No. 3.9e 0; Mismatches
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EMBL/GenBank/DDBJ
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Eli Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barliu J.F., Apbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Beros P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Beasu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Beasu A., Baxendale J., Borkstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Disk C., Dunn P.,
RA Gerbilds B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I., B., Davies P.,
RA Gerbilds B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gerbilds B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gerbilds B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gerbilds B., Coultiellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Neckohum K.A.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Harris N.L., Mattei B., McIntosh T.C., Krapitz S., Kalp D., Lai Z.,
RA Harris N.L., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. I.,
RA Kilmel B.E., Kodira C.D., Kraft C., Krapitz S., Kalp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Palazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palary G., Siden-Kiamos I., Stopleton M., Strong R., Sun E.,
RA Williams S.M., Woodaye T., Worley K.C., W
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Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
Ephydroidea; Drosophilidae; Drosophi
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Best Loc
Matches
AcGAP protein.
RACGAP50C OR CG13345.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inseptygota; Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
                                                                                                                                                                                        Q9N9Z9 PRELIMINARY;
Q9N9Z9;
Q1-CCT-2000 (TrEMBLrel. 1
Q1-CCT-2000 (TrEMBLrel. 1
Q1-JUN-2002 (TrEMBLrel. 2
ACGAP protein.
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Pfam; PF00130; DAG_PE_bind; 1.
Pfam; PF00620; RhoGAP: 1.
SMART; SM0109; C1; 1.
SMART; SM0109; C1; 1.
SMART; SM0124; RhoGAP: 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
PROSITE; PS50041; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50041; DAG_PE_BIND_DOM_2; 1.
SEQUENCE 625 AA; 69762 MW; 535F2CF986AA8F03
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InterPro; IPR002219; DAG_PB-bind.
InterPro; IPR0002198; RhoGAP.
InterPro; IPR000198; RhoGAP.
Pfam; PF00130; DAG_PB-bind; 1.
Pfam; PF00130; DAG_PB-bind; 1.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00109; C1; 1.
SMART; SM00109; C1; 1.
SMART; SM00109; C1; 1.
SMART; SM001324; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
SMART; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
PROSITE; PS000479; DAG_PE_BIND_DOM_2; 1.
SEQUENCE 625 AA; 69763 MW; E3892199534D19D0 C1
     Q9XUS9;
Q9XUS9;
01-NOV-1999
01-NOV-1999
01-DEC-2001
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; AJ251502; CAB96203.1; -.
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Cooperation between Ras and Rac signalling pathways
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Rhabditidae; Peloderinae;
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SEQUENCE 681 AA; 76314 MW; B3DD74F4CC51B68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the
   521
                                       543
                                                                       469
                                                                                                            484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282:2012-2018(1998).
                                                            NRDTLAFLMIHLQRV-AQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQ-----D
                                                                                                                                                                                                   LADFVSQTSPMIPSIVVHCVNEIEQRGLIETGLYRISGCDRTVKELKEKFLRVKTVPLLS
                                                                                                                                                                                                                                                                            VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIP-----TLIGTPVKIGEGM
                                                                                                                                                                                                                                                                                                                                                  YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKW------QRTDHELGKYKDLLM
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. A
                                                                                                                                            KVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEI--TDEDNSIAAMYQAVGELPQA
                                                                                                                                                                                                                                                        DKCATALKLA-TSMKCRDCHQVVHRSCCNKLHLPCIPRPKTMMTPKSALRGAKPGAGEFR
                                                                                                                                                                                                                                                                                                                             GQTTNNIGLGMSSAILTKSTLDIRTLKRGTPAWTNGTTR-DIAMRPHTFIEAGIKAMRKC
                                                                                                                                                                                                                                                                                                                                                                                                   CRDDGSTPHQEMTTTTTTTTTTTHNSRAQNQDPPRVSLHRQLTRRSLSCGSIPSCDQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRNGREVRRSSAAGNAVGGKRRSASAHAITAAANSKRSRSRVMTATIDEEPNEGGTPPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKK-REKRRSTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDRDQFKFLHE---PLVRTYSKRVQ--QRHPHLMEDTQDDEDDSEVDYDETGDSFEEVIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWD----SSLVKTFK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KARKKLAMFDIDVKDTQKHLRALMEENKALKLDLNVYETREKQLKDAMKNGIFNS--LTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSRHIFNMILNSQRPQFDIKDIGMFHLIDEIERLRKLWKDSEESKKRLNADMREAEEALA
 IKRQPKVVERLLSLPLEYWSQFMMVEQENIDPLHVIENSNAFSTPQTPD----
                                       NRDTLAYLFIHWRKVIAQSSRNKMNCEAMARMVAPAVMGH-----
                                                                                                         -LHDVEVITDTLKRFLRDLKDPLIPRTSRQELIVAANLYSTDPDNGRLALNRVICELPQA
                                                                                                                                                                              LQDFCTSAKPMIPAAVIHCVVALEARGLTQEGIYRVPGQVRTVNVLLDE-LRSKTVPNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                    TRSIGSAVDQGNESIVAKTTVT-----VPNDGGP-----IEAVSTIETVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 547.5; DB 5; Pred. No. 3.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B3DD74F4CC51B685 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQFVDGPPG----PVKK 200
                                     PVKQSQSQAIAGRD
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IKVSLLG
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                                                                                                                                            468
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RESULT
Q91V57
ID V9
AC Q9
DT 011
DT 011
DT 011
DT 011
DE 9e
OC Mal
OC Mal
OX NC
RN (11
RP SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                           Q91V57
Q91V57;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95VR1
Q95VR1;
Q1-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                     Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            gene).
                                                                                                                                           N-chimaerin
 STRAIN-ILS,
                SEQUENCE FROM N.A.
                                                    NCBI_TaxID=10090
                                                                                                                                                                                                                                                                        12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                        s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; (
                                                                                                                                                        (TrEMBLrel. 19, CTEMBLrel. 19, CTEMBLrel. 21, CTEMB
   AND
                                                                                                                                         (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 21, Last annotation update) (Unknown) (Protein for MGC:19150) (RIKE
                                                                                                                                                                                                                                   PRELIMINARY;
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ISS;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

(RIKEN

CDNA

1700112L09

Created)

PRT;

334

B

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Reineke A., Asgari S., Ma G.
"Sequence analysis and expre
VLP2, from the parasitic was
Submitted (AUG-2001) to the
EMBL; AF410773; AAL02015.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; In Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocr
Ichneumonoidea; Ichneumonidae; Campopleginae; Venturia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venturia canescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000198; RhoGAP. Pfam; PF00620; RhoGAP; 1. SEQUENCE 354 AA; 40074 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=32260;
                                                                                                                                                                                                                                                                                                                                                                361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
                                                                                                                                                                                                                                                                          421 LEKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
DPEDLSRYGNEEIDQDDPVYENVNLRSQTVNQGQPELLYAS
                                                                                                                         QFM---MVEQENIDPLHVIENSNAFS-TPQTPDIK----VSLLGPVTTPEHQLLKTPSSS
                                                                                                                                                              QRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWS
                                                                                                                                                                                                                                                                                                                                  MIPPLIIHCINAVELRGMTELGLYRLSGNKDRYEFLIQQFLKNDGALDLSEY-DIPTITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATDCHRAMTALFEFDDVYWQRFLGTSA---
                                                                                  KFIDPRKLQQRRLSELTRSQSSTQLSQLSRRPNLQGLSGSHALTPLSRPTEAAFKKRSSS
                                                                                                                                                                                                                                                ALKQFLRSLSEPLVTYALRDTFIEAAMLPDARDRDVELGSVVMQLPQANLDTLAYLMLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVTTPEHQLLKTPSSSSLSQRVRSTLTKNTPRFGS
                                      ---SLSQRVRSTLTKNTPRFGSKS--KSATNLGRQGNFFAS
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40074 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma G., Beck M., Schmidt O., expression of a virus-like particle ic wasp Venturia canescens."; the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Last sequence upo
, Last annotation on VLP2.
                                                                                                                                                                                                                                                                                                                                                                                                                    56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 431; DB 5;
Pred. No. 1.4e-21
6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7DC0949724316449 CRC64;
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    VSMASNQIETARHQDNFALCDRSILG

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                                           628
    280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein,
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                         540
                                                                                                                           592
                                                                                                                                                                    179
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RESULT 13
Q96FB0
ID Q96FB
AC Q96FE
DT 01-DJ
DT 01-DJ
DT 01-M
DE Simi
OS HOMM
OC EUK
OC EUK
CC MAM
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RA St
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Best Local S
Matches 91
                                                                                                                                                                                                                                                                                   Q96FB0;
01-DEC-2001 (TrEMBLrel. 19, Created
01-DEC-2001 (TrEMBLrel. 19, Last so
01-MAR-2002 (TrEMBLrel. 20, Last an
Similar to chimerin (chimaerin) 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Q96FB0
  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC011393; AAH11393.1; -
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J., Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.; "High-Throughput Sequence Identification of Gene Coding Variants within Alcohol-Related QTLs."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00520; RhoGAP; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1;
PROSITE; PS50081; DAG_PE_BIND_DOM_2;
SEQUENCE 334 AA; 38121 MW; 9EC5D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                         TISSUE=EYE;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000198; RhoGAP.
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Last annotation updat
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Pred. No. 1.4e-14;
46; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                Created)
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Catarrhini;
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                       Query Match
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                                                                                                                                         MEDLINE-92252621; PubMed-1374499; George J.M., Clayton D.F.;
"Differential regulation in the avian so predicting a highly conserved protein re the bcr oncogene."; Brain Res. 12:323-329(19 EMBL; S98891; AABZ2136.1; -. HSSP, P28867; IPTO. InterPro; IPRO02219; DAG_PE-bind. InterPro; IPRO02219; RhGAP.
                                     Piam; Privoco;
PRINTS; PRO0008; DAGPEDOMAIN.
PRINTS; SM00109; C1; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
                                                                                                                                                                                                                                                                                                                      Eukaryota; M
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Passeriformes; Passer Fringillidae; Carduelinae; Serinus. NCBI_TaxID=54072;
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Q92153;
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PROSITE; PS50081; DAG_PE_BIND_DOM_1;
PROSITE; PS50081; DAG_PE_BIND_DOM_2;
PROSITE; PS50001; SH2; 1.
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9.9%;
nilarity 31.6%;
Conservative 4:
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Last sequence update)
Last annotation updat
 Score 320; DB 13;
Pred. No. 4.3e-14;
7; Mismatches 106
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Pred. No. 5.7e-14;
B; Mismatches 117;
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Best Local Matches

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RESULT 15
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Best Local S
Matches 137
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--- SIMILARITY: TO OTHER EUKARYOTIC RHO GDP-DISSOCIATION II EMBL; AL035065; CAA22624.1; --
HSSP; Q07960; 1RGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative GTPase-activating protein C23G7.08C.
SPBC23G7.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00055; FCH; 1.
SMART; SM00324; RhoGAP; 1.
Hypothetical protein; GTPase activation.
DOMAIN 420 426 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001060; Cdc15_Fes_CIP4.
InterPro; IPR000198; RhoGAP.
Pfam; PF00611; FCH; 1.
Pfam; PF00620; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces
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                                                       179 KREKRRST--SRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIE----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 VHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLR--VKTVPLLSKVDDIHAICSLLKD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 9.5%; score 308; DB 3; L
al Similarity 23.7%; Pred. No. 9.2e-13;
137; Conservative 87; Mismatches 223;
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                                                                                                                                                                                                                                                                                           QRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE-QKSALAF------LNRGQPS 134
HEDNKNPTDASKTKIIQPPSSYGTGSSAGKTNPPVNPTI--KVTAAIPS---PLQNTNPA
                                                                                                                        SLIANYLRYTKLCESNTLLNGLTIRPQKPTPTNCGLQHALDNINANTDFVQYVLHA-SIK 318
                                                                                                                                                                                   SSNAGNKRLSTIDESGSILSDI------SFDKTDESLDWDSSLVKTFKLK
                                                                                                                                                                                                                                                    PKSNAQLTKLEDEARLKAENAESDMHSKIENAQNVQKQLLCIHRPNYIKQFFSLQREIES
                                                                                                                                                                                                                                                                                                                                                                                                                                       KDFEDFRKKWQRTDHE----LGKYKDLLMKAETE-RSALDVKLKHARNQVDVEIK---RR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695 AA;
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Search	Qy	Оу	Qy	Qy db	Qу	Qy Db
Search completed: July 3, 2003, 09:56:17	485 Q-SPHTKMDVANLAKVEGPTIVAHAVPNPDPVTMSQDIK 522 :	425 FLRNIKEDILITERINRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTIAFIMIHIQRVA 484 	371 NEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICSLLKD 424 ::::      :  :    :    :  :     528 SQVENEGLNLQGIYRVPSSSARVNMLRSQFENNPLLQLHTPEDYENDVHAVADLLKI 584	343PVKIGEGMLADFVSQTS	291 SKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGT- 342	233 VSTIETVPYWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFV 290

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// SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AB027/31	ABB50/5/	1200000	ARCOKKKO	ABG61872	ABB58723	AAG66505	ABB66573	AAM25391	AAU17333	AAB93466	ABB58077	AAG67552	AAG65821	ABP51281	AAB42926	AAY21700	ABG12190	AAU17313	ABB59717	ABG20843	AAY05781	AAP60303	ABG12188	AAB97911	AAB41660	ABG16794	ABG16793	AAW97809	AAG67553	AAY90268	AAW75995	AAM41445	AAM39659	ABB59247	AAM41833
MOVET HUMBH GTAGHO	-		Novel human diagno	ໝ			Drosophila melanbg		Novel signal trans		Drosophila melanog	Amino acid sequenc	RhoGAP domain from	Human MDDT SEQ ID	Human ORFX ORF2690	_	Novel human diagno	Novel signal trans	Drosophila melanog		Human myosin IXa.	Sequence encoded b		Human G-protein ac	n ORFX	1 human	Novel human diagno	Human GTPase regul	-	Human GTP-ase acti	GTPase activating		Human polypeptide	יסי	Human polypeptide

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CC Note: The sequence data for this patent did not form part of the printed CC specification.
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Wang Z
Zhou
                                                   MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
                                                                                                                                                              VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP
                  QRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLFLEEWS
                                                                                                                                                                                                 YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
                                                                                                                                                                                                           YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
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                                                                                                                                                   VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP
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Goodrich R,
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                               The invention relates to novel isolated lung small cell cancer antigen cc polynucleotides (I) and polypeptides (II) used in a method of detecting cc cancer in a patient. The method is optionally performed by cutilising oligonucleotides (III), where the biological sample cc from the patient is contacted with (III), detecting the amount of colynucleotide to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells cc expressing (II) is useful for stimulating and/or expanding T cells cc expressing (II) is useful for stimulating and/or expanding T cells cc expressing (II) is useful for stimulations to permit the stimulation cc and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the cc development of a cancer especially lung cancer in a patient. An observable and for inhibiting the development of cancer in a patient. Anulog407-AAUG9431 represent novel human lung small cell
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21-JUN-2000;
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Sequence
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                                                                                                                                                                                                                                                                                       Lung tumour polynucleotide and diagnosis of cancer especially
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                                                                               cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination co of an oligonucleotide comprises a sequence complementary to the cc complementary strand of a polynucleotide which comprises a 5'-end cc complementary to an oligonucleotide comprising a sequence, where the combination of cc oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of cc oligonucleotide comprises at least 15 nucleotides and the combination of ct the 5'-end sequence3'-end sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and cl quene therapy. The primers are useful for synthesising polynucleotides, cf articularly full-length cDNAs. The primers are also useful for the cdetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and call sequences; and AAH13629 to AAH13632 crepresent human cDNA sequences; and AAH3679 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length
comprises: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2001.
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Sugiyama T, Wakam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t invention describes primer sets for synthesising 5602 n cDNAs defined in the specification. Where a primer set (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 99JP-0248036.
; 99JP-0300253.
; 2000JP-0118776.
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A, Nagai K,
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                         polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate heematopoiesis; and in
                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of vaccination, testing and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                   The invention relates
                                                                                                                                                                                                                                                  Claim
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                bone, cartilage,
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26-JAN-2001;
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suppression
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                                                                                                                                                                                                                                                                                                                                                          Liu C,
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 and/or stimulation;
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99.2%;
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            and/or nerve tissue
                                                                                                                                                                                                                                                                                               range of human polypeptides, useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1182; DB Pred. No. 6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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sue growth or regeneration;
anti-inflammatory agents; and
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Matches 205
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating tell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                    Disclosure;
                                                                                                              New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                        WPI; 2001-656860/75.
N-PSDB; ABL12159.
                                                                                                                                                                                            Venter
                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                  Drosophila;
                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                  27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB68056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in treatment of leukaemias. AAU29510-AAU33304 represent the amino sequences of novel human secreted proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB68056 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIHLQRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMLQGHQGVQPKVVERLLFLG
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                                                                                                                                                                                                                                                                                                                                                                                developmental biology;
                                                                                   SEQ ID NO
                                                                                                                                                                                           Adams M,
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2000US-0614150
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                                                                                                                                                                                           PWD,
                                                                                                                    detection reagent for detecting for elucidating cell signalling
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Pred. No. 3.1e
3; Mismatches
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and cell-cell
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  WO200175067-A2
                         Homo sapiens
                                              Human; chromosome food supplement; m
                                                                                   Novel
                                                                                                                                 ABG14787;
                                                                                                                                                       ABG14787 standard;
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human diagnostic protein

#14778

medical in

imaging;

gene mapping; gene therapy;
maging; diagnostic; genetic

(first

entry)

Protein;

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Matches 228;
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                         ENSNAFSTPQT-----PDIKVSLLGPVTTP-----EHQLLKTPSSSS
                                                                                                                                                             SQWKDFANAVQNPDTKTAQDMLVKSVKQLPQANRDTLAFLILHFQRIAQCPVVLMPIDNI
                                                                                                                                                                              GLTEVGLYRLSSSEREYKALKEQFLRGKATPHLGNT-DIYVLCCCVKDFLRSLTEPLIPT
                                                                                                                                                                                                                                                                                 GLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTF
                                                                                                                                                                                                                                                                                                                        DCPVRCHIDCRYLLTVSCVPQ-TGTPTTKTMTGYVTDFAPSIAPMIPALIVHCVNEIEAR
                                                                                                                                                                                                                                                                                                                                                        DCRVVSHPECRDRCPLPCIPTLIGTP-VKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QGNESIVAKTTVTVPNDG-GPIEAVSTIETVPYWTRSRRKTGTLQPWNSDSTLNSRQL
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-TPATVIKRVPSNKNDLLSLYATPFKGGTIKKRKFYGTPPASA
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35.1%;
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Pred. No. 1.5e-63;
0; Mismatches 225;
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CC Note: The sequence data for this patent did not appear in the printed content of the pulpo with full products of the content of the printed content of the pulpo with pulpo and content of the pulpo with the pulpo and content of the pulpo with the pulpo and content of the pulpo with the pulpo and the pulpo and
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23-AUG-2000;
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bB; AAS78974.
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57; Conservative
               SKVDDIHAICSLLKDFLRNFKEPLLTFRLNKAFMEAAEITDEDNSISAMYQAVGELPQAN
                                     SKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQAN
                                                                                                                                                                                                                                                        CPLPCIPTLIGTPVKIG-----EGMLADFVSQTSPMIPSIVVHCVNEIEQ-----
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                                                                                                           IKKWTNDMNRHFSKEDIYAAKKHMKKCSSLPAIREMQIKTTMRYHLTPVRIAIIKKSGNN 4188
                                                                                                                                                                                                                                                                                                        TLEENLGNTIQVIGMGKDFMSKT----PKAMATKAKIDKWDLIKLKSFFC
                                                                                                                                                                                                                                                                                                                                                  TPQSNGGMRLH-----DFVSKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDR
                                                                                                                                                                                                           -----TAKETTIRVNRQPTEWEKIFATYSSD-----KGLISRIYNELKQIYKKKTNNP 4128
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                                                                                                                                                              -RGLTETGLY---
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 625; DB 22;
Pred. No. 4.3e-42;
                                                                                                                                                           -RISGCDR--TVKELKEK-FLRVKTVPLL-
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                                                   CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in generating antibodies states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC and supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (III). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC consistency of the mapping, identification of mutations CC and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and a sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution of a product of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 40589; 103pp; English
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23-AUG-2000;
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Query Match

19.18;

Score 618;

DB 22;

Length 665

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RESULT 9
ABG19904
ID ABG1
XX ABG1
AC ABG1
XX Huma
KW Huma
KW Food
XX Homc
XX Homc
XX Homc
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess beddingster.
                                                                                                                                                                                                                       Claim 20; SEQ ID No 50263; 103pp; English
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upplement; medical in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TAKETTIRVNRQPTEWEKIFATYSSD-----KGLISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      j; gene mapping; gene
imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---RGLTETGLY----RISGCDR--TVKELKEK-FLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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smatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; forensic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                    mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422
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Best Local Sim
Matches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                   Homo
                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                              11-OCT-2001.
                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                         Novel human
                                                                                                                                                                                                                                                                                                                  ABG13958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                     18-FEB-2002
                                                                                                                                                                                                                                                                                                                                              ABG13958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001
                                                                                                                                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PVTMSQDIKRQPKVVERLLSLPLEYW 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLTPVRIAIIKKSGNNSKVDDIHAICSLLKDFLRNFKEPLLTFRLNKAFMEAAEITDEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTVPLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSFFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIKD--LNVRPKTIKTLEENLGNTIQDIGMG-KDFMSKT---PKAMATKTKIDKWDLIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESCVPCGKRIKFGKLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIAAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYNELKQIYKKKTNNPIKKWTNDMNRHFSKEDIYAAKKHMKKCSSLPAIREMQIKTTMRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIG-----EGMLADFVSQTSPMIPSIVVH 368
                                                                                                                                                                                                                                                                                                                                                                                                                    PVTMLQDIKCQPKVVERLPSLPLEYW 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1086 AA;
                                                                                                                                                                                                                                                        diagnostic protein #13949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                       2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 618; DB
Pred. No. 1.8e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                              1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TAKETTIRVNRQPTEWEKIFATYSSD-----KGLISR
                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e 618; DB 22;
L. No: 1.8e-42;
Lismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                            forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
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Drmanac RT,

Liu

'n

Tang YT;

WPI;

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RESULT 11
AAM41833
ID AAM41
XX
AC AAM41
XX
DT 22-OC
XX
Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polypertide (II) sequences. (I) is useful as hybridisation probes, complymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The complete cc and gene mapping, and in recombinant production of (II). The complete cc complete complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 158
Human polypeptide SEQ ID NO
                                                                         22-OCT-2001
                                                                                                                                                                           AAM41833 standard; Protein; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
                                                                                                                                                                                                                                                                                                                                                         489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-639362/73.
DB; AAS78145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 WTRSRRKTGTLQPWNSDST-LNSR-----QLEPRTETDSVGTPQSNGGMRLH------DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   TKMNVANLAEVFGSTIVAHAVPNPEPVTMLQDIKCQPKVVERLPSLPLEYW
                                                                                                                                                                                                                                                                                                                            TKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYW 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSKT---PKAMATKTKIDKWDLIQLKSFFC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLAICRKL-KLDPFLTAYTKINSRWIKDLNIRPKT----IKTLEENLGITIQDIGMGKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTEWEKIFATYSSD-----KGLISRIYNELKQIYKKKTNNPIKKWTNDMNRHFSKEDIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EGMLADFVSQTSPMIPSIVVHCVNEIEQ-------RGLTETGLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKHMKKCSSLPAIREMQIKTTMRYHLTPVRIAIIKKSGNNSKVDDIHAICSLLKDFLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RISGCDR--TVKELKEK-FLRVKTVPLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 44317; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.1%; Score 618; DB 22; 45.0%; Pred. No. 1.9e-42; tive 39; Mismatches 70;
                     6764
                                                                                                                                                                           ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SKVDDIHAICSLLKDFLRN 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TAKETTIRVNRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              968
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Query Match
Best Local
                                                                                                                                                               Matches
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, ActivinyInhibin activity, chemotactic/chemokinetic activity, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                    C.N.S disorders.
Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; Calzheimer's; Parkinson's disease; Huntington's disease; haemosta amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                   specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
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QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-442253/47.
DB; AAI60989.
                                                                                                                                                               115;
64
                                     61
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                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC
                                                                                                  MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK
AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQ
                     AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQ
                                                                               MDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK
                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0653450.
2000US-0662191.
2000US-0693036.
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Wehrman T, X
Goodrich R,
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99.1%;
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                                                                                                                                                             Score 581; DB 22;
Pred. No. 6.5e-41;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                        form
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invent; useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                              Sequence
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11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                 specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 4533; 21pp + Sequence Listing; English.
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LTLENVVTWQRVLKVLLLMPAGFWSQFLEV
                        TMSQDIKRQPKVVERLLSLPLEYWSQFMMV 545
                                                                                                                  LKEKFLRVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSI
                                                                                                                                                                                                                               QSNGG-MRLHDFVSKT-VIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCI
                                                                         AAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPV 515
                                                                                                  LRRKLLRGKSTPHLGN-KDTHTLCCCVKDFLRQLVHPLIPIYHRRDFEEATRHEDRLAVE
                                                                                                                                                     PQPQIGTK----RGCLSDYAPRVAPMVPALIVHCVTEIEARGLQQEGLYRVSSTREKCKR
                                                                                                                                                                                                        QSHSGLLREHNFKIKSYYYNVGNCVHCRKRIRFAMASLRCRACPLRCHIGCCRQLTVNCI
                                                                                                                                                                                                                                                                                                                                                                                        (ABL01840-ABL16175) and the encoded
                                                                                                                                                                                                                                                                                                              384 AA;
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting for elucidating cell signalling
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Pred. No. 2.4e-31;
4; Mismatches 102
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259 STLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESCVPCGKRIKFGKLS--LKC

Matches Best Local Query Match

90;

Conservative

48;

Score 322; DB 22; Pred. No. 2.2e-18; 8; Mismatches 117;

Length Indels

26;

Gaps

8

Similarity

9.98;

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TRESULT 13
AAM39659
AWA AAM39
AWA AA
                                                                                                                                                              The invention is a constitution of the encoded polypeptides (AAM38642-AAM42213) with noorrupic, the encoded polypeptides (AAM38642-AAM42213) with noorrupic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assaws for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                {\tt C.N.S} disorders. Note: The sequence data for this patent did not form part of the printed
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03-AUG-2000;
14-SEP-2000;
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        Sequence
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N-PSDB; AAI58815.
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
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Zhou P,
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0598042.
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Wehrman T,
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Xue AJ,
nac RT;
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Yang Y,
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RESULT 14
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
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Wang
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25-APR-2000;
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)B; AAI60601.
                                                                             nucleic acids and polypeptides, useful as central nervous system injuries -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLNSEGLYRVSGFSDLIEDVKMAFDRDGEKADISVNMYEDINIITGALKLYFRDLPIPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLTETGLYRISGCDRTVKELKEKFLR--VKTVPLLSKVDDIHAICSLLKDFLRNLKEPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADCGLNVHKQCSKMVPNDCKPDLKHVK-KVYSCDLTTLVKAHTTKRPMVVDMCIREIESR
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                                                           SEQ ID NO 6376; 10078pp; English
                                                                                                                                                                                     2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0662191.
2000US-0693036.
2000US-07273444.
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'1 P,
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2000US-0552317.
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                                                                                                                                           Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressant;
                                                                                                                                   Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                    ID NO
                                                                                                                                                                                                                                                                                                                                                                         neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
                                                                                                                                 Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                    6376.
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                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy;
y; central nervous system;
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Yang
                                                                                     for treating
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AAW75995
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                25-FEB-1997;
                                                  27-AUG-1998
                                                                                               Domain
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                                  19-ғев-1998;
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system, such as peripheral nervous injuries, peripheral neuropathy localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders.
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                                                                                                                                                                                                                                                      GLTETGLYRISGCDRTVKELKEKFLR--VKTVPLLSKVDDIHAICSLLKDFLRNLKEPLL
NAENLGIVFGPTLMRS--PELDAMAALNDIRYQRLVVELLI 345
                                                   DVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLL 532
                                                                                                                                      TFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTK---M 491
                                                                                                                                                                                                                      GLNSEGLYRVSGFSDLIEDVKMAFDRDGEKADISVNMYEDINIITGALKLYFRDLPIPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ATLKENEQIPKYE----
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                                                                                                            TYDAYPKFIESAKIMDPDEQLETLHEALKLLPPAHCETLRYLMAHLKRV--TLHEKENLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KIHNFKVHTFRGPHWCEYCA-NFMWGLIAQGVKC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 322; DB 22; Pred. No. 2.3e-18;
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PARG; GTPase activating protein; GAP; PTPL1 polypeptide; phosphata Rho family signal transduction; cancer cell; proliferation; GAP do Ras-like GTPase; Rho; Rac; Cdc42; PDZ domain; signal transduction; Ras-like GTPase; Rho; Rac; Cdc42; PDZ domain; signal transduction; intracellular protein tyrosine phosphatase; mast cell secretion;
                                                                                                                                                                                                                                                                       pharmacological agent; modulator;
WO9837196-A1
                                                                                                                                                                                                                                                                                                                                                                                                          GTPase activating protein (GAP),
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                                                                                                            /note= "z
613..652
                                                                 /note=
                                                                                                                                                           Location/Qualifiers 193..509
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                                                                                      "cysteine-rich
                                               "GAP domain"
                                                                                                                                        "ZPH domain"
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phosphatase;

domain;

98WO-US03323.

(LUDW-) LUDWIG INST CANCER RES.

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CE Expression vectors comprising the PARG nucleic acid can be used to CC transform host cells for the recombinant production of the protein. The CC PARG polypeptides or complexes comprising PTPLI polypeptide having CC phosphatase activity (AAW7599) and PARG polypeptide can be administered CC to mammalian cells to reduce Rho family signal transduction. The PARG CC polypeptides can be administered to cancer cells to reduce proliferation (which is increased by Rho family signal transduction). Alternatively, CC dominant-negative variants of the polypeptide (e.g. with a GAP domain CC inactivated) can be used to increase Rho family signal transduction.

CC PARG was determined to have GAP activity in vitro, which was strongest on CC Rho but also detected on Ras-like GTPases, Rac and Cdc42, and bound CC PARG ficially to the fourth PDZ domain (PDZ4) of known intracellular CC protein tyrosine phosphatase PTPL1, involved in signal transduction. CC PARG golypeptides and polynucleotides are useful to produce modulators of CC modulate mast cell secretion. The polypeptides are also useful for conduction or conduction pharmacological agents useful for disease diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This represents a human GTPase activating protein (GAP), PARG. The specification states that the unique PARG nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide, PARG, with GTPase activating activity - useful e.g. therapeutically to reduce Rho family signal transduction so reduce cancer cell proliferation, modulate mast cell secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Pages 41-48; 93pp; English.
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N-PSDB; AAV55846.
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                                            407
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                                                                                                                                                                                                                                                                                            242 WTRSRRKTGTLQPWNSDSTLNSRQLEPRTET--DSVGTPQS---NGGMRLHDFVSKTVIK 296
                                                                                                                                                                                                                                                                                                                                                                   182 KRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVPY 241
                                                                                                                                                                                                                                                                                                                                                                                                                               483
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                                                                                                                                                                                                                                                                                                                                             540. DSEST-----GGSSESRSLDS-----ESI-----SPGD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 VTVNLFHMQHLQAASLADRLQSLCGSAKLYDPGQEYSEFVKATNS----TEEEKVDGNV 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 RRIEEEALQKVE----EADELYKV-CVTNVEERRNDVENTKREILAQLRTLVFQCDLTLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 LDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEEQK---SA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
PLLSKVD------DI-----HAICSLLKDFLRNLKEPLLTFRLNRAFMEAAE----ITDE 451
                                                                                                         --AEFTLVAKKEPDGIPFILKICASEIENRALCLQGIYRVCG-----NKIKTE
                                                                                                                                                                                                               PESCYPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPC----IP---TLIGTPVKIGEG
                                                                                                                                                                                                                                                           FHRKLPRTPSSGTMSSADDLDEREPPSPSETGPNSLGTFKKTLMSKAALTHKF---RKLRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAFLNRGQPSSSNAGNKRLSTI---DESGSILSDISFDKTDESLDWDSSLVKTFKLKKRE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHE-LGKYKDLLMKAETERSA
                                                                                                                                                                       PTKCRDCEGIVVF -- QGVECEECLLVCHRKCLENLVIICGHQKLPGKIHLFG-----
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	949 SFEESERKQNALGK 962	дb	
	600 STLTKNTPREGSKSKSATNLGR 621	Qy	
948	889 SLQPQDVMCSIGVVDQGCFPKPLLSPEERDIERSMKSLFFSSKEDIHTSESESKIFERAT 948	Db	
599	544 -MVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTPSSSSLSQRVR 599	Оу	
888	837 MNSKNLGVIFGPSLIRPRPQTAPITISSLAEYSNQARLVEFLITYSQKIFDG 888	, Db	
543	491 MDVANLAKVEGETIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWSQEM 543	Qy	
836	777 QETKKNSLEDKKWPNMCIEINRILLKSKDLLRQLPASNFNSLHFLIVHLKRVVDHAEENK 836	οь	
490	452 DNSIAAMYQAVGELPQANRDTLAFLMIHLQRVA-QSPHTK 490	Qy	

Search completed: July Job time : 76 secs 3, 2003, 09:54:08

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                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printe and is derived by analysis of the total score distribution.
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1 MDTMMLNVRNLFEQLVRRVE.....SKSATNLGRQGNFFASPMLK 632
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F02569_2 protein (	hypothetical prote	GTPase-activator p	hypothetical prote	hypothetical prote	ralA-binding prote	hypothetical prote	KIAA0672.protein [	RalBP1 - rat	hypothetical prote	Rho GTPase activat	RhoGAP/LIM domain	KIAA1204 protein [	hypothetical prote	hypothetical prote	hypothetical prote

## ALIGNMENTS

RESULT 1  DESIGN 1  REC GTPRESE activating protein 1 (imported) - human  C.Species: Home sapiens (man)  R.Kawashima, T.; Kitamura, T.; Nesska, T.; Hitose, K.  R.Kawashima, T.; Nesska, T.; Hitose, K.  R.Kawashima, T.;		ALLUMENTS
Rac Cippase activating protein 1 [imported] - human C:Species Homo aspicas (man) C:Date: 03-uun 2002 sequence_revision 03-Jun-2002 stext_change 19-Jul-2002 C:Accession: D940 C:Accession: D940 R:Kawashimary, T: Kiramura, T: Mosska, T:; Hirose, K. Submitted to Genank. December 1999 A:Description: Homo aspicans Rac Grpase activating protein 1 (RACGAP1), mRNA. A:Residence number: D5430 A:Status: preliminary A:Accession: D940 A:Status: preliminary A:Accession: D940 A:Status: preliminary A:Cross-references: GB:NP_037409; PID:g7019433; PIDN:NP_037409.1  Query Match A:Cross-references: GB:NP_037409; PID:g7019433; PIDN:NP_037409.1  Query Match Best Local Similarity 100 0%; Predd No. 1 9e-18; Best Local Similarity 100 0%; P		RESULT 1 .
C:Species: Homo sappless (man) C:Species: Lo-Jun-2002 #sequence_revision 03-Jun-2002 *text_change 19-Jul-2002 C:Accession: D59430 C:Accession: D59430 C:Accession: D59440 A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens Rac GyPase activating protein 1 (RACGAP1), mRNA. A:Description: Homo sapiens RacGaption: Homo sapiens RacGaptio		1 [imported] -
C; Accession: DSy430  R; Kawashima, T; Kitamura, T; Nosaka, T; Hirose, K.  Submitted to GenBank, December 1999  A; Description: Homo sapions Rac GTPase activating protein 1 (RACGAP1), mRNA.  A; Reference number: D59430  A; Reference number: D59430  A; Status: preliminary A; A; Rasiduse: 1632 cKaM> A; Cross references: GB:NP_037409; PID:97019433; PIDN:NP_037409.1  Query Match  100.0%; Pred. No. 1.9e-198;  Best Local Similarity 100.0%; Pred. No. 1.9e-198;  Best Local Similarity 100.0%; Pred. No. 1.9e-198;  Best Local Similarity 100.0%; Pred. No. 1.19e-198;  Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps  1		<pre>#sequence_revision 03-Jun-2002 #text_change</pre>
A.Description: Isomo aspidans, Descender 1999 A.Description: Isomo aspidans Rac GTPASSE activating protein 1 (RACGAP1), mRNA. A.Reference number: D59430 A.A.Residues: D59430 A.A.Residues: Preliminary A.M.Status: Preliminary A.M.Status: Preliminary A.A.Residues: D59430 A.A.Residues: D59430 A.A.Residues: D59430 A.A.Residues: D59430 A.COSS Teferences: GB:NP_037409; PID:97019433; PIDN:NP_037409:1 A.Residues: D59430 A.COSS Teferences: GB:NP_037409; PID:97019433; DB 2; Length 632; Best Local Similarity 100.0%; Score 3243; DB 2; Length 632; Best Local Similarity 100.0%; Proprietion of D595 Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps  1		C; Accession: D59430 R; Kawashima, T.; Kitamura, T.; Nosaka, T.; Hirose, K.
A;SECULE: PREININGY A;Molecule type: mRNA A;Molecule type: mRNA A;Rosidues: 1-52 < KARA A;Rosidues: 1-		sapiens Rac GTPase activating protein 1 (RACGAP1), D59430
A:Cross-reterences: GB:NP_037409; PID:g7019433; PIDN:NP_037409.1  Ouery Match 100.0%; Score 3243; DB 2: Length 632; Best Local Similarity 100.0%; Pred. No. 1.9e-198; Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps  Oy 1 MDTWMLNVRNLFEQLVERKVEILSEGNEVOFIQLAKDFEDFRKKWQRTDHELGKYKDLIMK 60  INDIMALNVRNLFEQLVERKVEILSEGNEVOFIQLAKDFEDFRKKWQRTDHELGKYKDLIMK 60  OY 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE 12  OY 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE 12  OY 121 OKSALAFLARGQPSSSNAGNKELSTIDESGSILSDISFDKTDESLOMDSSLVKTFKLKKR 18  OY 122 OKSALAFLARGQPSSSNAGNKELSTIDESGSILSDISFDKTDESLOMDSSLVKTFKLKKR 18  OY 181 EKRRSTSRQFVDGPPGVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP 24		A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-632 <kaw></kaw>
QUEST MATCH  Best Local Similarity 100.0%; Pred. No. 1.9e-198;  Best Local Similarity 100.0%; Pred. No. 1.9e-198;  Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps  Qy 1 MDTMALAVRALFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK 60  ATTERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLACDTSGSIGLSEE 12  Db 11	ed,	A;Cross-references: GB:NP_037409; PID:g7019433; PIDN:NP_037409.1
Oy  1 MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK		100.0%, Decel 1042; 100.0%, Pred. No. 1.9e-198; vative 0; Mismatches 0; Indels 0; Gaps
Db I MUTHILLEQUERRULES ENERGY ED FOR		1 MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK
Qy 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIOLIREMIMCDTSGSIOLSEE	+	1 MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK
Db 61 AFFERSALDVELKHARNQVESKTARGRABADCEKLERQITQLIREMLINDTUSEE  Qy 121 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR  QY 121 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR  Db 122 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR  QY 181 EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP  Db 181 EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP  QY 241 YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC  QY 241 YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC  QY 301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP  Db 301 VPCGKRIKFGKLSLKCRDCRVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP  QY 361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS	prote	61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMIMCDTSGSIQLSEE
Qy 121 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR	ting	61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE
Db 121 QKSALAFINGQPSSNAGMRLSTIDETGLISTSTORTUSLIKKR  Oy 181 EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP	imila .	121 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLVKTFKLKKR
Qy 181 EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP	human	121 QKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWDSSLYKTFKLKKR
Db 181 EKRRITSRÖGVDGPFGPVKKTTSIGSANDGARESIVAKTTVTVPNNGGPILAVSTLETVP  Qy 241 YWTRSRRKTGFLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC	se ac	181 EKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETTVP
Qy 241 YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC	ra ra	181 EKRRSTSRQFYDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP
Db 241 YWTRSTRKTGTLQPWNSD\$TLNSRQLEPRTETD\$YGTPQSNGGNRLDDFV\$KTVLXPESC  Qy 301 VPCGKRIKFGKLSLKCRDCRVVSHPECDRCPLPCLPTLLGTPVKIGEGMLADFV\$QTSp	n, ce	241 YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDEVSKTVIKPESC
Qy 301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP	tor a	241 YMTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDEVSKTVIKPESC
Db 301 VPCGKRIKENIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	otein tivat	301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSP
Qy 361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS	nu .	301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADEVSQTSP
Db 361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS  Qy 421 LLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHL	n - C	361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
OY 421 LIKDFLRNIKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHL	prote	361 MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;McMurray, A.
submitted to the EMBL Data
A;Reference number: Z19743
A;Accession: T23454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K08E3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T23454
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; Residues: 1-681 <WIL>
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Best Local :
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                                                                          LQDFCTSAKPMIPAAVIHCVVALEARGLTQEGIYRVPGQVRTVNVLLDE-LRSKTVPNVG
                                                                                        LADFYSQTSPMIPSIVYHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLS
                                                                                                                               DKCATALKLA-TSMKCRDCHQVVHRSCCNKLHLPCIPRPKTMMTPKSALRGAKPGAGEFR
                                                                                                                                                              VPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIP-----TLIGTPVKIGEGM
                                                                                                                                                                                           GQTTNNIGLGMSSAILTKSTLDIRTLKRGTPAWTNGTTR-DIAMRPHTFIEAGIKAMRKC
                                                                                                                                                                                                                        YWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESC
                                                                                                                                                                                                                                                   CRDDGSTPHQEMTTTTTTTTTTHNSRAQNQDPPRVSLHRQLTRRSLSCGSIPSCDQTP
                                                                                                                                                                                                                                                                                TRSIGSAVDQGNESIVAKTTVT-----VPNDGGP-
                                                                                                                                                                                                                                                                                                           LRNGREVRRSSAAGNAVGGKRRSASAHAITAAANSKRSRSRVMTATIDEEPNEGGTPPKR
                                                                                                                                                                                                                                                                                                                                           LKK-REKRRSTS----
                                                                                                                                                                                                                                                                                                                                                                     EDRDQFKFLHE---PLVRTYSKRVQ--QRHPHLMEDTQDDEDDSEVDYDETGDSFEEVIH 186
                                                                                                                                                                                                                                                                                                                                                                                                 EQKSALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDESLDWD---SSLVKTFK 176
                                                                                                                                                                                                                                                                                                                                                                                                                               KARKKLAMFDIDVKDTQKHLRALMEENKALKLDLNVYETREKQLKDAMKNGIFNS--LTK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSRHIFNMILNSQRPQFDIKDIGMFHLIDEIERLRKLWKDSEESKKRLNADMREAEEALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKW-----QRTDHELGKYKDLLM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLTKNTPRFGSKSKSATNLGRQGNFFASPMLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237/3; 361/3; 612/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 547.5; DB 2; Pred. No. 4.8e-27;
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                                                                      C;Accession: A48122
R;Agnel, M.; Roder, L.; Vola, C.; Griffin-Shea, R.
Mol. Cell. Biol. 12, 5111-5122, 1992
A;Title: A Drosophila rotund transcript expressed during A;Reference number: A48122; MUID:93024458; PMID:1406685
A;Accession: A48122
A; Note: sequence C; Genetics:
                           A; Molecule type: nucleic acid
A; Residues: 1-384 <AGN>
                                                                                                                                                           GTPase-activating protein Rac homolog, splice form C;Species: Drosophila melanogaster C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994
                                                                                                                                                                                                        RESULT
A48122
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GTPase-activating
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A;Molecule type: nucleic acid
A;Residues: 1-383 <AGN>
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C; Date: 21-Jan-1994 #sequence_revision
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A;Cross-references: FlyBase:FBgn0003263
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Best Local S
Matches 110
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23-Feb-1997

spermatogenesis and

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NCBIP:115661)

clone

pc1.7

fruit fly (Drosophil

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C;Accession: B48122
R;Agnel, M.; Roder, L.; Vola, C.; Griffin-Shea, R.
Mol. Cell. Biol. 12, 5111-5122, 1992
A;Title: A Drosophila rotund transcript expressed during
A;Reference number: A48122; MUID:93024458; PMID:1406685
A;Accession: B48122
LTLENVVTWQRVLKVLLLMPAGFWSQFLEV 336
                                                                                                                  AAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPV 515
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                                             TMSQDIKRQPKVVERLLSLPLEYWSQFMMV 545
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                                                                                             MAVYLAVLELHQAHRDTLAYLMLHWQKIAESPAVRMTVNNLAVIFAPTLFG----
                                                                                                                                                                                     LRRKLLRGKSTPHLGN-KDTHTLCCCVKDFLRQLVHPLIPIYHRRDFEEATRHEDRLAVE 252
                                                                                                                                                                                                                                LKEKFLRVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSI
                                                                                                                                                                                                                                                                                PQPQIGTK----RGCLSDYAPRVAPMVPALIVHCVTEIEARGLQQEGLYRVSSTREKCKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 477; DB 2;
Pred. No. 6.5e-23;
4; Mismatches 102;
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F;239-246/Region: nucleotide-binding motif A (P-loop)
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1980 <REI>A;Residues: 1-1980 <REI>A;Cross-references: EMBL:X77609; NID:g639998; PIDN:CAA54700.1; PID:g639999 A;Cross-references: EMBL:X77609; NID:g639998; PIDN:CAA54700.1; PID:g639999 A;Cross-references: EMBL:X77609; PID:g639998; PIDN:CAA54700.1; PID:g639999 A;Cross-references: PID:g639998; PIDN:CAA54700.1; PID:g639999 A;Cross-references: PIDN:CAA54700.1; PID:g63999 A;Cross-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, EMBO J. 14, 697-704, 1995
A;Title: A novel type of myosin implicated in signalling by rhc A;Reference number: S54307; MUID:95188874; PMID:7882973
A;Accession: S54307
A;Status: preliminary; nucleic acid sequence not shown
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C;Speckes: Rattus norvegicus (Norway rat)
C;Date: 15-7ul-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S54307
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A;Cross-references: FlyBase:FBgn0003263
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{\tt TMYSVPNGKIHVGYKDLMENYQIVVSNLAAERGEKDTNLVLNVFQSLLDEFTRSYNKT-D}
                                                                                         TIETVP-----
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                                                                                                                                                                   GQITVSEKWRESVFRKITNANELKFLDEFLLNKVNDLRSQKTPIESLFIEATERFRSNIK
                                                                                                                                                                                                                                                                                                                         HKAKDKKPSLEGVEETEGSGGQAAQEAPARKTLDVPSSQQHRHTTGEKPLKGKKNRNRKV
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22.1%;
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Pred. No. 1e-13;
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J. Cell Sci. 109, 653-661, 1996
A;Title: Human myosin-Txb, an unconventional myosin with a chimerin-like rho/rac A;Reference number: A59256; MUID:97063843; PMID:8907710
A;Accession: A59256
                                                                                                                                                                                                                                                                                             A;Map position: 19p13.1
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C;C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C;C;Keywords: nucleotide binding; P-loop
E;149-941/Domain: myosin motor domain homology #status atypical <MMO>
E;239-246/Region: nucleotide-binding motif A (P-loop)
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A;Residues: 1-2022 <MIR>
A;Cross-references: GB:U42391; NID:g1147782; PIDN:AAC50402.1; PID:g1147783
A;Cross-references: GB:U42391; NID:g1147782; PIDN:AAC50402.1; PID:g1147783
R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin
A;Reference number: A55758; MUID:94294418; PMID:8022818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin-IXb [similarity] - human (Species: Homo sapiens (man) (M
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A; Map position: 19p13.1
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A; Residues: 234-322 <
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    1404 LSPGSQVDSKSTFKRLFLHKTKD-----KKYSLEGAEELENAVSGHVVLEATTMKKGLEA 1458
                                                                                 22 LSEGNEVQ-----FIQLAKDFEDFRKKWQ---RTDHELGKYKDLLMKAETERSALDV 70
                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A-QSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWSQF
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                                                                                                                                                               Conservative
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23.0%;
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                                                                                                                                                                                                                                        Score 334;
                                                                                                                                                                                                           Pred.
                                                                                                                                                                   Mismatches
                                                                                                                                                                                                           NO.
                                                                                                                                                                                                       8.3e-13;
                                                                                                                                                                                                                                    Length 2022;
                                                                                                                                                                   Indels
                                                                                                                                                                   116;
                                                                                                                                                               Gaps
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GTPa

1907

585

629

1849 542 483 1732 423 1675

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N-chimerin - rat

N;Alternate names: GTPase-activating protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 08-Oct-1999
C;Accession: S29128; S25152
R;Lim, H.H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.
Biochem. J. 287, 415-422, 1992
A;Title: Developmental regulation and neuronal expression of the mRNA of ra
*Reference number: S29128; MUID:93074974; PMID:1445199
                                                                 A;Cross references: EMBL:X67250; NID:g55939; PIDN:CAA47672.1; PID:g55940 R;Lim, H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C. submitted to the EMBL Data Library, July 1992
A;Description: Rat n-Chimaerin a p2Irac GAP:CDNA sequence developmental r A;Reference number: S25152
A;Reference number: S25152
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-334 <LIMBL:
A;Residues: 1-334 SIMBL:
A;Cross-references: EMBL:X67250; NID:g55939; PIDN:CAA47672.1; PID:g55940
C;Superfamily: protein kinase C zinc-binding repeat homology <KZZ>F;81-130/Domain: protein kinase C zinc-binding repeat homology <KZZ>
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Residues: 1-334 <LIM>
     Matches
                     Local
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YWSQFMMVEQENIDPLHVIEN-----SNAESTPQTPD-----IKVSLLGPVT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLVKVALLEDVNRMSPGALAIIFAPCLL-RCPDNSDPLTSMKDVLKITTCVEMLIKEQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLQRVA-QSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLE 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGVLKQWLRELPEPLMTFAQYGDFLRAVELPEKQEQLAAIYAVLEHLPEANHNSLERLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPIVLEKLLEHVEMHGLYTEGLYRKSGAANRTRELRO---ALQTDPAAVKLENFPIHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDD--IHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYIWLMDKALLCSVCKMTCHKKCVHKIQSHCSYTYGRKGEPGAEPGHFGVCVDSLTSDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTL--IGTP-VKIGE-GMLADFVSQTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYTK-----NDFEPVKQSKAQKKKRKQERAVQEHNG----HVFASYQVSIPQSCEQCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIKTMYSVPNGKI----HVGYKDLMENYQIVVSNLATERGQKDTNLVLNLFQSLLDEFTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RQITNAN----ELKYLDEFLLNKINDLRSQKTP---
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   Conservative
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                   10.18;
 46;
                                    Score 329;
                     Pred. No. 1.4e-13;
 Mismatches
                                      DB 2;
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                                      Length 334
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 26;
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S08242
N-chimerin
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J. Mol. Bi
               N-chimerin - common canary
N;Alternate names: protein kinase C homolog [misidentification];
C;Species: Serinus canaria (common canary)
C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 0
C;Accession: A43953
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R;George, J.M.;
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Matches 90
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Res. D.F. 12,

323-329,

04-Feb-2000

song control

circuit

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A;Cross-references: EMBL:X51408; NID:g35012; PIDN:CAA35769.1; PID:g35013 C;Superfamily: protein kinase C zinc-binding repeat homology F;46-95/Domain: protein kinase C zinc-binding repeat homology <KZ2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hall, C.; Monfries, C.; Smith, P.; Lim, H.H.; Kozma, R.; Ahme J. Mol. Biol. 211, 11-16, 1990 A;Title: Novel human brain cDNA encoding a 34,000 M(r) protein A;Reference number: S08242; MUID:90133942; PMID:2299665 A;Accession: S08242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-299 <HAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Alternate names: GTPase-activating protein
;Species: Homo sapiens (man)
;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
NAENLGIVFGPTLMRS--PELDAMAALNDIRYQRLVVELLI
                                                   DVANLAKVEGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLL
                                                                                                                                                                                                                                                                                                                                          ADCGLNVHKQCSKMVPNDCKPDLKHVK-KVYSCDLTTLVKAHTTKRPMVVDMCIREIESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATLKENEQIPKYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESCVPCGKRIKFGKLS--LKC
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                                                                                                               TYDAYPKFIESAKIMDPDEQLETLHEALKLLPPAHCETLRYLMAHLKRV--TLHEKENLM
                                                                                                                                                                     TFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTK---M
                                                                                                                                                                                                                              GLNSEGLYRVSGFSDLIEDVKMAFDRDGEKADISVNMYEDINIITGALKLYFRDLPIPLI
                                                                                                                                                                                                                                                                                 GLTETGLYRISGCDRTVKELKEKFLR--VKTVPLLSKVDDIHAICSLLKDFLRNLKEPLL 434
                                                                                                                                                                                                                                                                                                                                                                                                   RDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADCGLNVHKQCSKMVPNDCKPDLKHVK-KVYSCDLTTLVKAHITKRPMVVDMCIREIESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQR 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.9%;
ilarity 32.0%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 322; DB 2;
Pred. No. 3.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KIHNFKVHTFRGPHWCEYCA-NFMWGLIAQGVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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   292
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R;Xiang, Z.; Aves, S.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, January 1999
A;Reference number: Z21893
A;Accession: T39954
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: Type: DNA
A;Status: 1-695 <XIA>
A;Cross-references: EMBL:AL035065; PIDN:CAA22624.1; GSPDB:GN00067; A;Cross-references: strain 972h-; cosmid c23G7
C;Genetics:
A;Gene: SpDB:SPBC23G7.08c
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Differential regulation in the avian song control circuit of A;Reference number: A43953; MUID:92252621; PMID:1374499
A;Accession: A43953
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T39954
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A;Experimental source: HVC-associated telencephalon
A;Note: sequence extracted from NCBI backbone (NCBIN:98891, NCBIP:98892)
C;Superfamily: protein Kinase C zinc-binding repeat homology
F;46-95/Domain: protein kinase C zinc-binding repeat homology <KZ2>
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C;Accession: T39954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable gtpase activating protein homolog - fission yeast (Schizosaccharomyces
C; Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
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Best Local Similarity
Matches 92; Conserve
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A; Residues: 1-299 <GEO>
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                           260
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137; Conserv
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                                                                                                                                              QRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE-QKSALAF------LNRGQPS
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                                                                                                                                                                                                    KSIKEYAKKQENAYLEAVMQMDKSKSRFKGAETEYNRALDNK-----NTGDSQKKVGFFK
                                                                                                                                                                                                                                          KDFEDFRKKWQRTDHE----LGKYKDLLMKAETE-RSALDVKLKHARNQVDVEIK---RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKADISVNMYEDINIITGALKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDCRVVSHPECRDRCPLPCIPTL-----IGTPVKIGEGMLADFVSQTSPMIPSIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESCVPCGKRIKFGKLS--LKC 316
  KREKRRST--SRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIE----A
                                       SLIANYLRYTKLCESNTLLNGLTIRPQKPTPTNCGLQHALDNINANTDFVQYVLHA-SIK
                                                                                   SSNAGNKRLSTIDESGSILSDI
                                                                                                                     PKSNAQLTKLEDEARLKAENAESDMHSKIENAQNVQKQLLCIHRPNYIKQFFSLQREIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSPHTK---MDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADCGLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVK-----AHFTKR-----PMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TLHEKENLMSAENLGIVFGPTLM---RAPELDAMAALNDIRYQRLVVEMLI 292
                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 4.4e-13;
7; Mismatches 106
                                                                                                                                                                                                                                                                                                      Score 308; DB 2; Pred. No. 8.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KVHNFKVHTFRGPHWCEYCA-NFMWGLIAQGVKC
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                 -SFDKTDESLDWDSSLVKTFKLK 178
                                                                                                                                                                                                                                                                                                                         Length 695
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                                                                                                                                                                                                                                                                                 Indels 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Saras, J.; Franzen, P.; Aspenstrom, P.; Hellman, U.; Gonez, L.J.; submitted to GenBank, December 1997
A;Description: Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA A;Reference number: E59430
A;Accession: E59430
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
E59430
E79430
E79420
C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1261 <SAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 9.3%; Score 301; DB 2;
Similarity 22.4%; Pred. No. 5.4e-11;
53; Conservative 120; Mismatches 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E59430
  MLADF--VSQTSP-MIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTV 406
                                       PTKCRDCEGIVVF - - QGVECEECLLVCHRKCLENLVIICGHQKLPGKIHLFG-----
                                                                               PESCYPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPC----IP---TLIGTPVKIGEG
                                                                                                                       FHRKLPRTPSSGTMSSADDLDEREPPSPSETGPNSLGTFKKTLMSKAALTHKF---RKLRS
                                                                                                                                              KRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVPY
                                                                                                                                                                                                                                                                                 NKHLNSSQPSGFGPANSLEDVVRLPDSSNKIEEDRCSNSADIT----GPSFIRSWTFGMFS
                                                                                                                                                                                                                                                                                                                         LAFLNRGQPSSSNAGNKRLSTI---DESGSILSDISFDKTDESLDWDSSLVKTFKLKKRE 181
                                                                                                                                                                                                                                                                                                                                                                                                    LDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEEQK---SA
                                                                                                                                                                                                                                                                                                                                                                                                                                              RRLEEEALQKVE---EADELYKV-CVTNVEERRNDVENTKREILAQLRTLVFQCDLTLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNLFEQLYRRYEILSEGNEVQFIQLAKDFEDFRKKWQRTDHE-LGKYKDLLMKAETERSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENSDVNKMSTNNLAIIWGPTIIKQAT-IPEISSFSRTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFRELREPLIPDNHQRDFIDAGNVEDESRRRDAVHRAINDLPDANYSTIRHLTIHLAKIK
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C;Superfamily: protein kinase C zinc-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: sequence extracted from NCBI backbone (NCBIP:125731) R;Leung, T.; How, B.E.; Manser, E.; Lim, L. submitted to the EMBL Data Library, November 1992 A;Description: Germ cell beta-chimaerin, a new GTPase-activa A;Reference number: S31398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: GTPase-activating protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A45485; S31398; S29956
R;Leung, T; How, B.E.; Manser, E; Lim, L.
J. Biol. Chem. 268, 3813-3816, 1993
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A; Residues: 1-295 <LE2>
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A; Title: Germ cell beta-chimaerin, a new GTPase-activating protein
A; Reference number: A45485; MUID:93179371; PMID:8440677
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  EAVHEVLMLLPPAHYETLRYLMIHLKKVTMNEKDNLMNAENLGIVFGPTLM--RPPEDST
                                          AAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTK-MDVANLAKVFGPTIVAHAVPNPDP
                                                                                                                                   VKTVPLLSKVD
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                                                                                                                                                                                                          PVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLR 402
                                                                                                                                                                                                                                                               KTHNFKVHTFRGPHWCEYCA-NFMWGLIAQGVRCSDCGLNVHKQCSKHVPNDCQPDLKRI 98
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                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                  Score 294; DB 2;
Pred. No. 1.9e-11;
2; Mismatches 111
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                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: A53764
R;Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 269, 12888-12892, 1994
A;Title: (Cerebellar betaz-chimaerin, a GTPase-activating protein A;Title: (Cerebellar betaz-chimaerin, a GTPase-activating protein A;Reference number: A53764; MUID:94230370; PMID:8175705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 269, 12888-12892, 1994
A;Title: Cerebellar beta2-chimaerin, a GTPase-activating A;Reference number: A53764; MUID:94230370; PMID:8175705
A;Recession: B53764
                                                                                                        A; Molecule type: mRNA
A; Residues: 1-466 <LEU>
A; Residues: 1-466 <LEU>
A; Cross-references: GB:L29126; NID:g457229; PIDN:AAA19191.1; PID:g457230
A; Cross-references: GB:L29126; NID:g457229; PIDN:AAA19191.1; PID:g457230
C; Superfamily: protein kinase C zinc-binding repeat homology; SH2 homology
F; 57-137/Domain: SH2 homology <SH2>
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A; Residues: 1-443 <LEU>
C; Superfamily: protein |
F; 34-114/Domain: SH2 hor
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N;Alternate names: GTPase-activating protein
C;Species: Rattus norvegicus (Norway rat)
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C;Accession: B53764
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                                                                                    213-262/Domain: protein
Matches
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                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTHNFKVHTFRGPHWCEYCA-NFMWGLIAQGVRCSDCGLNVHKQCSKHVPNDCQPDLKRI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLHDFVSKTVIKPESCVPCGKRIKFGKLS--LKCRDCRVVSHPECRDRCPLPCIPTLIGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAVHEVLMLLPPAHYETLRYLMIHLKKVTMNEKDNLMNAENLGIVFGPTLM--RPPEDST 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTK-MDVANLAKVFGPTIVAHAVPNPDP 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTTLHDMRYQKLIVQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKTVPLLSKVD-----DIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSI 455
  Conservative
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                    9.1%;
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                                                                                    kinase C zinc-binding repeat homology <KZ2>
  66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C
                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 294; DB 2;
Pred. No. 3.4e-11;
2; Mismatches 111
                                          Score 293.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zinc-binding repeat homology
ed. No. 4e-11;
Mismatches 1
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                                          DB 2;
  155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 443;
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                                              466;
  63;
                                                                                                                                                                                                                                                                                                                                                                        21-Jul-2000
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
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12;

Db 81 EELDLRL-IRTKGGVDAALEYAKTWSRYAKELLAWTEKRASYELE Qy 68 LDVK	9435 9435 9435  m-interacting protein [imported] - Species: Homo sapiens (man) Date: 03-Jun-2002 #sequence_revisi Accession: D59435 Aresta, S.; Beranger, F.; Berger, Dmitted to GenBank, November 2000 Description: GMIP, a Gem interacti Reference number: D59435 Accession: D59435 Status: preliminary Molecule type: DNA Residues: 1-970 <are> Cross-references: GB:NP_057657; P1 Guery Match Best Local Similarity 22.6%; Pr Matches 188; Conservative 112;</are>	Db  116 KREESIHDLVTDGLITLYIETKAAEYISKMTTNPIYEHIGYATL  Qy  253 QPWNSDSTLNSRQLEPRTETDSVGTPQSNGGM
EELDLRL-IRTKGGVDAALEVAKTWSRVAKELLAWTEKRASYELEFAKSTMKIAEAGKVS 139  LDVK	2002 #text_change 19-Jul-2002 zburg, J. ; PIDN:NP_057657.1 DB 2; Length 970; se 273; Indels 260; Gaps	

. 698	817 HPTATPTEIPTPOSDOREDVAEDTKDGGGEVSSQGPEDSLLGTOSRGHFSRQP 869	ДЪ
629	597 RVRSTLTK-NTPRFGSKSKSATN	Qy
HSTLEQ 816	761 ELPQATEPPPQDFSPAPGPLTTSSQPPPPHLDPDSQPPVLASDPGPDPQHHSTLEQ	Db
SSSLSQ 596	555 VIENSNAFSTPQTPDIKVSLLGPVTTPEHQLLKTPSSSSLSQ	Qy
EQIFGMD 760	717 TLLRPPDGPRAASAIPVTCLLDSGHQAQLVEFLIVHYEQIFGMD 760	DЪ
ENIDPLH 554	503 TIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYMSQFMMVEQENIDPLH 554	Qy
GIVEGP 716	657 DPGTPSPSPDVIRSLKTLLVQLPDSNYNTLRHLVAHLFRVAARFMENKMSANN	Db
LAKVEGP 502	453NSIAAMYQAVGELPQANRDTLAFLMIHLQRV-AQSPHTKMDVANLAKVFGP 502	Qy
LHADPGD 656	598 LCQAFENGRALVELSG-NSPHDVSSVLKRFLQELTEPVIPFHLYDAFISLAKTLHADPGD 656	рь
IDED 452	396 LKEKFLRVKTVPLLSKYDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDED 452	QУ
SRVRVER 597	543 PARTPL-FGVDELQLPRDEPEEVPEVVTKCTAEIEHRALDVQGIYRVSGSRVRVER 597	Db
CDRTVKE 395	341GTPVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKE 395	. Qy
LCGHRRL 542	483 GKWTLSSAAQTHQLRRLRGPAKCRECEAFMVSGTECEECFLTCHKRCLETLLILCGHRRL 542	· Db
340	310 GKLSL	Qy
NGLGSPF 482	423 VDSVGGGSESRSLDSPTSSPGAGTRQLVKASSTGTESSDDFEERDPDLGDGLENGLGSPF 482	Db
CGKRIKF 309		Qy

Search completed: July 3, 2003, 09:57:41 Job time: 46 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MDTMMLNVRNLFEQLVRRVE.....SKSATNLGRQGNFFASPMLK 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112892 seqs, 41476328 residues
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RN_DROME
MY9B_RAT
MY9B_MOUSE
CHIN_HOUSE
CHIN_HOUSE
CHIN_HUMAN
CHIO_HUMAN
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OPHL_HUMAN
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OPHL_HUMAN
RAGH_HUMAN
RHGB_HUMAN
RGD1_YEAST
YLE5_CAEEL
YAU9_SCHPO
RHG4_HUMAN
RGD1_YEAST
YAU9_SCHPO
RHG4_HUMAN
RGB_HUMAN
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054834
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P38339
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Q9nsg0
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Q9y313
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P39083
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                                                                                                                                                                                                            P52757
                                                                                                                                                                                                                                                                               P40809 drosophila
                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                       Q63358 rattus norv
       homo sapien
saccharomyc
caenorhabdi
schizosacch
homo sapien
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rattus norv
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45	44	43	42	41	40	39	38	37	36	35	34	
128.5	128.5	129	130.5	130.5	132	132.5	134	135	135	137	137.5	
4.0	4.0	4.0	4.0	4.0	4.1	4.1	4.1	4.2	4.2	4.2	4.2	
1616	878	1505	3685	1080	705	724	988	3678	1395	724	3093	
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P200_MYCGE	KPCO_HUMAN	CUT1_HUMAN	DMD_HUMAN	HDA4_CHICK	YNP9_CAEEL	P85A_BOVIN	PCK1_SCHPO	DMD_MOUSE	CUT1_MOUSE:	P85B_BOVIN	POLG_BSTV1	
Q49429 mycoplasma	Q9bz16 homo sapier	P39880 homo sapier	P11532 homo sapier	P83038 gallus gall	P34562 caenorhabdi	P23727 bos taurus	P36582 schizosacch	P11531 mus musculu	P53564 mus musculu	P23726 bos taurus	Q65730 b genome po	

## ALIGNMENTS

ite)  ite)  ite)  ite)  ite)  ite)  ite)  ite)  ite)  itera: Brachycera;  prosophila.  R;  prosophila.  R;  prosophila.  R;  iffin-Shea R;  ilanogaster rotundRacGAP  ilanogas
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA She B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yen, Y.H., Zhong F.N., Zhou N., Zhang G., Zhao Q., Zheng L.,
RA Yen, Y.H., Zhong F.N., Zhou N., Zhang G., Zhao Q., Zheng L.,
RA Yeney X.H., Zhong F.N., Zhou N., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhou S., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                               VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                               PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.

Guanine-nucleotide releasing factor; Spermatogenesis; Testis; Alternative splicing; Zinc; Phorbol-ester binding.

DOMAIN 87 136 PHORBOL-ESTER AND DAG BINDING.

DOMAIN 188 202 ARG/LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF000130; DAG_PE-bind; 1.
Pfam; PF000620; RhoGAP; 1.
SMART; SM00109; C1; 1.
SMART; SM00324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Us entities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M99702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0045843; rnRacGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: IN UPDAE, EXPRESSED IN IMAGINAL DISH
IN THE MALE GONAD. IN ADULTS, ONLY FOUND IN THE TESTES,
FILLED WITH PRIMARY SPERMATOCYTES.
DEVELOPMENTAL STAGE: EXPRESSED DURING SPERMATOGENESIS, 1
SPERMATOCYTES, AND IMAGINAL DISK MORPHOGENESIS.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN. CAUTION: IT IS UNCERTAIN WHETHER MET-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN THE MORPHOGENESIS OF THE ADULT GTPASE-ACTIVATING PROTEIN FOR P21-RAC. PROMOTES THE E RAC-BOUND GUP BY GTP.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A48122; A48122
                                                                                                                                                279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U22539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration
   396
                                                                           337
                                      138
                                                                                                                                                                                         110;
                                                                                                                78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE003672;
                                                                                                                                                                                                          Similarity
                                                        P-TLIGTPVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKE
                                                                                                              QSHSGLLREHNFKIKSYYYNVGNCVHCRKRIRFAMASLRCRACPLRCHIGCCRQLTVNCI.
                                                                                                                                                QSNGG-MRLHDFVSKT-VIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCI
LKEKFLRVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSI
                                        PQPQIGTK---
                                                                                                                                                                                                                                                                                                                                                                                              PS00479; DAG_PE_BIND_DOM_1; 1.
                                                                                                                                                                                                                                                               378
384 AA;
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                               202 F
384 P
44217 MW;
                                                                                                                                                                                                        14.78;
40.78;
                                      RGCLSDYAPRVAPMVPALIVHCVTEIEARGLQQEGLYRVSSTREKCKR
                                                                                                                                                                                       44;
                                                                                                                                                                                                       Score 477; DB 1
Pred. No. 2e-23;
                                                                                                                                                                                                                                                               NLSSTHL -> RPMVSL
; D24959B833B7A2A8
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ong as its content is in
                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR MET-23 IS THE INITIATOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
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                                                                                                                                                                                     Gaps
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RESULT 2
MY9B_RAT
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16-OCT-2001 (R
16-OCT-2001 (R
16-OCT-1001 (R
MYOSIN IXD (UN
MYO9B OR MYR5.
                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MY9B_RAT
Q63358;
                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                          InterPro; IPR000198; RhoGAP.
InterPro; IPR001609; myosin_head
Pfam; PF00063; myosin_head; 2.
Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                          EMBL; X77609; CAA54700.1; -. HSSP; P08799; 1MND.
                                                                                                                                                                                                                        or send an
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                             -i- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, LUNG, THYMI
LIVER, AND SPLEEN.
-i- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                 Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reinhard J., Scheel A.A., Diekmann D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE-Brain MEDLINE=95188874; PubMed=7882973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            InterPro;
                                                                                                                                            InterPro;
                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baehler M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.

MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.

ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.

ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON CHO.

SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS LOCALIZION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE PERINUCLEAR REGION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                        BINDING DOMAIN.
SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOSIMILARITY: CONTAINS 4 IQ DOMAINS.
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PR00193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTKMDVANLAKVFGPTIVAHAVPNPDPV 515
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IPR000048; IQ_region.
IPR000159; RA_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                        email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Unconventional myosin-9b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of myosin
                RΑ;
                               RhoGAP;
                                               ĮQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
 MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40, Created)
40, Last sequence 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    implicated in signalling
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                                                                                                                                                                                                                                                                                                                                                                 GLOBULAR HEAD DOMAIN
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                                                                                                                                                                                                                                        . Usage by and for commercial
http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinal
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Best Local
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SMART; SM00105; IQ; 3.
SMART; SM00242; MYSG; 1.
SMART; SM00314; RA; 1.
SMART; SM00314; RhoGAP; 1.
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NP_BIND
SEQUENCE
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                                                                                                               424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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 MMVEQENIDPLHVIEN----
                                                                                                                                                 VVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDD--IHAICSLLK 423
                                                                                                                                                                                                                                                                                                                                                            G--SAVDQGNESIVAKTT------VTVPND----GGPIEA-----VS
                                                                                                                                                                                                                                                                                                                                                                                                                                  TSDVSKLSPVKTSTEVDGDLSAKKPAGHKKKSEDPSAGPDAGLPTGSQGDSKSAFKRLFL 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAGNKRLSTIDESGSILSDISFDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIKRRQRAEADCEKLERQIQLIR--EMLMCDTSGSIQLSEEQKSALAFLNRGQP---SSS
                                                                                                                                     LEKLLEHVEMHGLYTEGLYRKSGAANRTRELRQ---ALQTDPATVKLEDFPIHAITGVLK
                                                                                                                                                                                    KALLCSVCKMTCHKKCVHKIQSYCSYTGRRKSELGAEPGHF--GVCVDSLTSDKASVPIV
                                                                                                                                                                                                           LSLKCRDCRVVSHPECRDRCPLPCIPT-----LIGTPVKIGEGMLADFVSQTSPMIPSI 365
                                                                                                                                                                                                                                     FEPVKGKAQKKKRKQERAVQ
                                                                                                                                                                                                                                                             LQPWNSDSTLNSRQLEPRTETDSVGTPQSNGGMRLHDFVSKTVIKPESCVPCGKRIKFGK 311
                                                                                                                                                                                                                                                                                    TMYSVPNGKIHVGYKDLMENYQIVVSNLAAERGEKDTNLVLNVFQSLLDEFTRSYNKT-D 1568
                                                                                                                                                                                                                                                                                                              TIETVP--
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                                  ALLEDVNRMSPGALATIFAPCLL-RCPDNSDPLTSMKDVLKITTCVEMLIKEQMRKYK--
                                                            A-QSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWSQF
                                                                                    QWLRELPEPLMTFAQYGDFLRAVELPEKQEQLAAIYAVLDHLPEANHTSLERLIFHLVKV
                                                                                                          DFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRV
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1046
1841
1918
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958
981
1002
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1045
1980
1861
1948
856
978
1001
1024
1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g; Calmodulin-binding; Actin-binding;
GTPase activation; Phorbol-ester binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAIL.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

ACTIN-BINDING.

IQ 1.

IQ 2.

IQ 3.

IQ 3.

IQ 4.

PHORBOL-ESTER AND DAG BINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 348; DB 1; 1
Pred. No. 3.3e-14;
5; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHO-GAP.
ATP (POTENTIAL).
W; D79FEC4D0FAE0C05 CRC64;
                                                                                                                                                                                                                                   -----EHNG----HVFASYQVNIPQSCEQCLSYIWLMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q Q
SNA-----FSTPQTPDIKVSLLGPVTTPEHQL
                                                                                                                                                                                                                                                                                                                                                                                                            -TSRQFVDGP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1980
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RESULT 3

MY9B_MM
AC 090Y06
DT 16-OCT
DT 26-OCT
RT 26-OC
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MYO9B OR MYR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 240:389-398(1995).

Gene 240:389-398(1995).

Gene 240:389-398(1995).

Gene 240:389-398(1995).

Gene 240:389-398(1995).

Gene 240:389-398(1995).

ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.

MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS

ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP

AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.

ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.

-I- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH

F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS

LOCALIZTION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE

PERINUCLEAR REGION (BY SIMILIARTY).

-I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/Q AND 3/C ARE

PRODUCED BY ALTERNATIVE SPLICING.

-I- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN, HEART, MUSCLE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grewal P.K., Jones
                                                                                              InterPro; IPR002219; DAG_PE-bind InterPro; IPR000048; IQ_region. InterPro; IPR000159; RA_domain.
                                                                                                                                                                                                               MGD; MGI:106624; Myo9b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of the murine unconventional myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20047919; PubMed=10580159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLO SIMILARITY: CONTAINS 4 IQ DOMAINS.
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                                                                                                                                                                                                                                                                                                      AF143687;
AF143685;
AF143686;
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                                                                                                                                                                                                                                       P08799; 1MND
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                                                                  IPR000048; IQ_regi
IPR000159; RA_doma
IPR000198; RhoGAP.
   IPR001609; myosin_head
)063; myosin_head; 2.
                                                                                                                                                                                                                                                                                                      AAF00120.1;
AAF00121.1;
                                                                                                                                                                                                                                                                          AAF00118.1;
                                                                                                                                                                                                                                                                                                                                                                                AAF00122.1;
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                                                                                                                                                                                                                                                                                                             ALT_FRAME
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SEQUENCE
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PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50096; IQ; 3.
Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
Cytoskeleton; Coiled coil; GTPase activation; Phorbol-ester binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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PF00612;
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SM00015;
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SM00324; RhoGAP; 1.
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SM00109; C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00193;
                                                                                                                                                                                                                                                                           Similarity
                                                         FLLNKVNDLRSQKTPIESLFIEATERFRSNIKTMYSVPNGKIHVGYKDLMENYQIVVSNL
                                                                                                                                                                                                  MCDTSGSIQLSEEQK---SALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDK----
                                                                                                                                                                                                                       ESPKDKD---KDESSTKAQD---KPESPSGSTQIQRYQ--HPDTERLATAVEIWRGKKLA
                                                                                                                                                                                                                                           ELGKYKDLLMKAETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIR--EML
                                                                                                 ARKTLDVPSSQQHRHTTGEKPLKGKKNRNRKVGQITVSEKWRESVFRKITNANELKFLDE 1475
                                                                                                                                           KKKSGDPSAGPDAGLSPGSQGDSKSAFKRLFLHKAKDKKPSLEGVEETESNGGQAAQETP
                                                                                                                                                                                SAVLSQSLDLSEKHRATGAALTPTEERRISFSTSDISKLSPVKTSAEIDGDFSSKKPSIH
SNGGMRLHDFVSKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPT-
                  AAERGEKDTNLVLNVFQSLLDEFTRSYNKT-----DFERAKSKAQKKKRKQERAV---Q
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ACTIN-BINDING.
10 1.
10 2.
10 3.
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PHORBOL-ESTER AND DAG BIND
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                                                                                                                                                                                                                                                                                                         M.
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Pred. No. 1.3e-13;
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GPDAPALPCPISTLSPLPEAAAAPPRGRPTSFVTVRVKTPR
RTPINEMANIKLPPGLPLHLTSWAPALQEAVVPVKRREPPA
RRQDQVHSVYIAPGADLPSQSTLIALDHDTILPGTKRRYSD
PPTYCLPPSSGQANG -> E (IN ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POT
R -> RCT
ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAD OR MOTOR DOMAIN.
NECK OR REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                          C57B1/6; CONTAINS AN IN IMPERFECT DUPLICATION).
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                                                                                                                                                                                                                                                                Mismatches
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RESULT 4
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            EMBL; x67250;
PIR; S25152; S
PIR; S29128; S
HSSP; P28867;
                                                                                                                                                                                                                                                                                                     n-chimaerin, a p21rac GAP:cDNA sequence.";
Biochem. J. 287:415-422(1992).
-i- FUNCTION: GTPASE ACTIVATING PROTEIN FOR P21-RAC
ESTER RECEPTOR. MAY PLAY AN IMPORTANT ROLE IN NE
TRANSDUCTION MECHANISMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
N-chimaerin (NC) (N-chimerin) (Alpha chimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIN_RAT P30337;
                                                                                   use by non-profit institu
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entities requires a license
or send an email to license@
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Wistar; TISSUE-Brain;
MEDLINE-93074974; PubMed-1445199;
Lim H.H., Michael G.J., Smith P., Lim L., Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                               *Developmental regulation and neuronal expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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                                                                                                                                                                                                                               TISSUE SPECIFICITY: IN NEURONS IN BRAIN REGIONS IN LEARNING AND MEMORY PROCESSES.
DEVELOPMENTAL STAGE: INCREASES IN AMOUNT DURING COINCIDENT WITH SYMAPTOGENESIS.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ES
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                                        ; CAA47672.1;
S25152.
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                                                                                   license@isb-sib.ch).
                                                                                                                               institutions as long
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                                                                                                agreement (See http://www.isb-sib.ch/announce/
                                                                                                            is not removed
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InterPro;

IPR002219;

DAG\_PE-bind

S29128.

1PTQ

InterPro; IPR000198; RhoGAP

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15-JUN-2002
15-JUN-2002
                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
GTPASE activation; Phorbol-ester borbol-ester DOMAIN
81 130 PHORBOL-ESTER
DOMAIN 157 303 RHO-GAP.
SEQUENCE 334 AA; 38210 MW; D7F828C6368
                                                                                                                                                                                                                                                                                                                       Beeson M., Gordon L., Bennett B., Johnson "High-throughput sequence identification within alcohol-related OTLs.";
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ILS, and ISS;
Ehringer M.A., Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHNI
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                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE-Colon, and
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                               SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
                      SWISS-PROT entry
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                                                                                                                                                                                                                                                                                                       (DEC-2000)
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(NC) (N-chimerin) (Alpha chimerin
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Bennett B., Johnson
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Pred. No. 4.6e-14;
6; Mismatches 118
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D7F828C63683528B CRC64;
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Sciurognathi; Muridae;
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Jht. It is produced through a description of the EMBL
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Sikela J.
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; Murinae; Mus
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    a collaboration
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PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.

GTPase activation; Phorbol-ester binding;
DOMAIN 81 130 PHORBOL-PERMONENT 157 200
                                                                                                                                                                                                                                                                                                                 MY09B OR MYKD.

HOMO Sapiens (Human).

Homo sapiens (Human).

Herota; Metazoa; Chordata;

Heria; Primates;
                                                                                                                   TISSUE-Liver, and Small intestine;
MEDLINE-97063843; PubMed-8907710;
Wirth J.A., Jensen K.A., Post P.L., Bement W.M.,
"Human myosin-IXb, an unconventional myosin with
rho/rac GTPase-activating protein domain in its t
J. Cell Sci. 109:653-661(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                               MY9B_HUMAN STANDARD; PRT; 2158 AA (2013459; Q9UHN0; 075314; Q9UUJ2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Myosin IXb (Unconventional myosin-9b).
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EMBL; BC024/96; AAH24/96.1; -.
EMBL; BC025023; AAH25023.1; -.
Interpro- Teenonno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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InterPro; IPR000198; RhoGAP.
Pfam; PF00130; DAG_PE-bind; 1.
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                           Grewal
                                               PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE MEDLINE=20047919; PubMed=10580159;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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AF332070;
BC010825;
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38121 MW;
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                           Maconochie
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Pred. No. 5.4e-14;
6; Mismatches 118
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                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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tent is in
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RI SUDMITTED TO THE COLL SERVE IN THE ABSENCE WITH ATPASE CC -1- FUNCTION: MYOSINS ARE ACTIV-BASED MOTOR MOLECULES WITH ATPASE CC -1- FUNCTION: MYOSINS ARE ACTIV-BASED MOTOR MOLECULES WITH ATPASE CC ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTERACELLULAR MOVEMENTS. CC MAY BE INVOLVED IN THE REMODELING OF THE ACTIV CYTOSKELETON. BINDS CC ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATPACE AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS. CC ALSO ACTS AS A GIPASE ACTIVATING PROTEIN ON RHO.

CC -1- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS ITS CC FACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS CC FACTIN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS CC PERINUCLEAR REGION.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN PERIPHERAL BLOOD INTEVNAL SELECTIVE INVESTED TO THE METATIVE SPECIFIC AND A TOWER SERVERSED PREDOMINANTLY IN PERIPHERAL BLOOD INTEVNAL SELECTIVE INVESTED TO THE METATIVE SPECIFIC STREETS AND A THEY MAY SELECTIVE SPECIFICITY. EXPRESSED PREDOMINANTLY IN PERIPHERAL BLOOD INTEVNAL SELECTIVE INVESTED SELECTIVE SPECIFICITY.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00109; C1; 1.
SMART; SM00015; IQ; 3.
SMART; SM00242; MYSC; 1.
                                                                                                                  Pfam;
Pfam;
Pfam;
                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                          EMBL; U42391; AAC50402.1; ALT_SEQ.
EMBL; B4143684; AAF00119.1; -.
EMBL; AF020267; AAC26597.1; -.
EMBL; AK002201; BAA92132.1; ALT_IN
                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzi
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori I
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kas
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari
                                                                                                                                                                                  InterPro: IPR000048: IQ_region.
InterPro: IPR000159; RA_domain.
InterPro: IPR000189; RhogAp.
InterPro: IPR001609; myosin_head
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                                                                                              m; PF00063; myosin_head; 2
mm; PF00130; DAG_PE-bind; 1
m; PF00612; IQ; 4.
m; PF00620; RhoGAP; 1.
m; PF00788; RA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING DOMAIN.

SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD

SIMILARITY: CONTAINS 4 IQ DOMAINS.

CAUTION: THE C-TERMINAL SEQUENCE FROM AA 1917 ONW

WAS PROBABLY A CHIMERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEUKOCYTES AND AT LOWER LEVELS, IN THYMUS, SPIEEN, I PROSTATE, OVARY, BRAIN, SMALL INTESTINE, AND LUNG. SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER
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                                                                                                                                                                                                                                                                                           HGNC:7609; MYO9B.
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., Bokoch G.M., Mooseker M.S.;
yosin-IXb is a mechanochemically active
                                                                                                                                                                                                                                                        IPR002219; DAG_PE-bind
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       -FSTPQTPDIKVSLLGPVTT
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93330292; PubMed-8336731;
Hall C., Sin W.C., Teo M., Michael G.J.; Smith P., Dong J.M.,
Lim H.H., Manser E., Spurr N.K., Jones T.A., Lim L.;
"Alpha 2-chimerin, an SH2-containing GTPase-activating protei
the ras-related protein p21rac derived by alternate splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93074974; PubMed-1445199;
Lim H.H., Michael G.J., Smith P., Lim L., Hall C.;
"Developmental regulation and neuronal expression n-chimaerin, a p21rac GAP:CDNA sequence.";
Biochem. J. 287:415-422(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hall C., Monfries C., Smith P., Lim H.H., Kozma R., Ahmed S., Vanniasingham V., Leung T., Lim L.; "Novel human brain cDNA encoding a 34,000 Mr protein n-chimaerin, related to both the regulatory domain of protein kinase C and BCR the product of the breakpoint cluster region gene."; J. Mol. Biol. 211:11-16(1990).
                                                                         PHORBOL-ESTER BINDING.
MEDLINE=91097509; PubMed=2268301;
Ahmed S., Kozma R., Monfries C.,
                                                                                                                                                Dong J.M., Smith P., Hall C., Lim L.;
"Promoter region of the transcriptional unit for human chimaerin, a neuron-specific GTPase-activating protein Eur. J. Blochem. 227:636-646(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                     receptor.
                                                                                                                                                                                                                                TISSUE=F1broblast;
MEDLINE=95172046; PubMed=7867622;
                                                                                                                                                                                                                                                                                                                                                                                                                                          human n-chimerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
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                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-1)
                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to
                                                                                                                                                                                                                                                                                                                                                 TISSUE-Eye;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                           "Human brain n-chimaerin
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 FUNCTION: GTPASE ACTIVATING PROTEIN FOR P21-RAC AND A PHORBOL
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                                                                                                                                                                                                                                                                                                                               R.
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                         272:767-773(1990)
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                                                           ries C., Hall cDNA encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                            selectively expressed
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or send an email to license@isb-sib.ch).
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DOMAIN
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ProDom; PD000093; SH2; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1;
PROSITE; PS50081; DAG_PE_BIND_DOM_2;
PROSITE; PS50001; SH2; 1.
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EMBL; Z22641; CAA80354.1; -.
EMBL; BC011393; AAH11393.1; -.
EMBL; S75654; AAB33506.1; -.
PIR; S08242; S08242.
HSSP; P28867; 1PTQ.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002219; DAG
InterPro; IPR000198; Rho
InterPro; IPR000980; SH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: IN NEURONS IN BRAIN REGIONS THAT
IN LEARNING AND MEMORY PROCESSES.
DEVELOPMENTAL STAGE: INCREASES IN AMOUNT DURING BRAIL
COINCIDENT WITH SYNAPTOGENESIS.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING DOMAIN.
SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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PF00017; SH2; 1.
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TFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQSPHTK---M
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                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                       Score 322; DB 1
Pred. No. 2e-13;
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RPKYYGREFHGMISREAADQLLIVAEGSYLIRESQRQPGTY
TLALRFGSQTRNFRLYYDGKHFVGEKRFESIHDLVTDGLIT
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                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                           Length 459;
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Q03070;
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                                                                                                            PRINTS; PR00008; DAGPEDOMAIN. SMART; SM00109; C1; 1. SMART; SM00324; RhGGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         <del>-</del> -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00479; DAG_PE_BIND_DOM_1; PROSITE; PS50081; DAG_PE_BIND_DOM_2;
                                                                                                                                                                                   EMBL; X69489; CAA49244.1; -. EMBL; L07494; AAA40809.1; -. HSSP; P28867; LPTQ.
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in rat testis.";
J. Biol. Chem. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Wistar; TISSUE=Testis; MEDLINE=93179371; PubMed=8440677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                          SEQUENCE
                                                                      Alternative splicing.
                                                                                GTPase activation; Phorbol-ester binding;
                                                                                                                                             Pfam; PF00130; DAG_PE-bind; 1. Pfam; PF00620; RhoGAP; 1.
                                                                                                                                                                InterPro; IPR002219; DAG_PE-bind InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                    entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                     the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHN2 OR BCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-chimaerin (Beta-chimerin).
                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                ARE PRODUCED BY ALTERNATIVE SPLICING. THE CEREBELLAR FORM CONTAINS A SH2 DOMAIN.

TISSUE SPECIFICITY: FOUND IN CEREBELLUM AND TESTIS.

DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN LATE S

SPERMATOCYTES. IN THE CEREBELLUM, EMERGENCE OF BETA-2

COINCIDES WITH GRANULE CELLS MATURATION AND EXHIBITS

DEVELOPMENTAL INCREASES. EXPRESSION IS SPECIFICALLY R
                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       JIOI. Chem. 268:3813-3816(1993).
FUNCTION: GTPASE ACTIVATING PROTEIN FOR P21-RAC.
SUBCELLULAR LOCATION: Membrane-associated (Potential).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                        BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 ZINC-DEPENDENT
                                                                                                                                                                                                                                                                                                                                         WEAVER MUTANT.
                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414
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            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAENLGIVFGPTLMRS---PELDAMAALNDIRYQRLVVELLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLL
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  Conservative
                                                    118
                                          À,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                         262
33837
                                                               91
           9.1%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
                                          MW;
  52;
           Score 294; DB 1
Pred. No. 6.7e-1
                                                            PHORBOL-ESTER
                                                    RHO-GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                         D7692D957B4816BD
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                     DB 1;
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                                                                                Zinc; Membrane;
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                                                             AND
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GENCE OF BETA-2 ISOFORM
N AND EXHIBITS POSTNATAL
SPECIFICALLY REDUCED IN
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                                                             DAG
                   Length 295;
                                         CRC64;
  Indels
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BETA-2
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  32;
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CHIO_HUMAN
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Strong C., Graves T., Yoakum M., Hawkins M.;
submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

FUNCTION: GTPASE ACTIVATING PROTEIN FOR P21-RAC. INSUFFICIENT

EXPRESSION OF BETA-2 CHIMAERIN IS EXPECTED TO LEAD TO HIGHER RAC

ACTIVITY AND COULD THEREFORE PLAY A ROLE IN THE PROGRESSION FROM

LOW-GRADE TO HIGH-GRADE TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95339337; PubMed=7614486;
Yuan S.; Miller D.W., Barnett G.H., Hahn J.F., Williams B.R.G.;
"Identification and characterization of human beta 2-chimaerin:
association with malignant transformation in astrocytoma.";
Cancer Res. 55:3456-3461(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Cerebellum;

MEDLINE-94230370; PubMed-8175705;

Leung T., How B.-E., Manser E., Lim L.;

Leung T. How B.-E., Manser E., Lim L.;

"Cerebellar beta 2-chimaerin, a GTPase-activating protein ras-related rac is specifically expressed in granule cells unique N-terminal SH2 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIO_HUMAN
P52757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 18-192 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain; MEDLINE=95339337; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606
                                                                           ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGEST LEVELS IN THE BRAIN AND PANCREAS.
EXPRESSED IN THE HEART, PLACENTA, AND WEAKLY IN THE KIDNEY ALLIVER. EXPRESSION IS MUCH REDUCED IN THE MALICNANT GLIOMAS,
COMPARED TO NORMAL BRAIN OR LOW-GRADE ASTROCYTOMAS.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
     SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Membrane-associated (Potential). ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 AND BETA-2 (S
                                                           BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR BCH.
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RHO-GAP DOMAIN.
SH2 DOMAIN.
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RESULT 10
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Best Local
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PRODOM; PD000093; SH2; 1.
SMART; SM00109; C1; 1.
SMART; SM00109; C1; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1
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CONFLICT
OPHL_HUMAN STANDARD; PRT; 814 AA. Q9UNA1; O75117; Q9UJOO; Q9BYS6; Q9BYS7;
                                                                                                                                                                                                                                                                                                                                                                       GTPase active splicing.
Alternative splicing.
59 127
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Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00620; RhoGAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                             Similarity
                                                     <u>٥</u>---
                                                                     ERLLSLPLEYWSQFMMVEQENI 550
                                                                                               RDTLAFLMIHLQRVAQSPHTK-MDVANLAKVEGPTIVAHAVPNPDPVTMSQDIKRQPKVV 528
                                                                                                                       NYYPDINITGALKLYERDLPIPVITYDTYSKFIDAAKISNADERLEAVHEVLMLLPPAH
                                                                                                                                  TTLVKAHNTQRPMVVDICIREIEARGLKSEGLYRVSGFTEHIEDVKMAFDRDGEKADISA
                                                                                                                                                                           ADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLR--VKTVPLL
                                                                                                                                                                                           FRGPHWCEYCA-NFMWGLIAQGVRCSDCGLNVHKQCSKHVPNDCQPDLKRIK-KVYCCDL
                                                                                                                                                                                                           VIKPESCVPCGKRIKFGKLS--LKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGML
                                                                                                                                                                                                                               ----SRRLSRSKNEPRKTNVTHEEHTAVEKISSLVRRAALTHNDNHFNYEKTHNFKVHT
                                                                                                                                                                                                                                               QPWNSDSTLNSRQLEPR-----TETDSVGTPQSNGGM------RLHDFVSKT
                                                                                                                                                                                                                                                                 KRFESIHDLVTDGLITLYIETKAA-----EYISKMTTNPIYEHIGYATLLREKV---
                                                                                                                                                                                                                                                                                   KKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVP-----YWTRSRRKTGTL
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                                                                                      YETLRYLMIHLKKVTMNEKDNFMNAENLGIVFGPTLM--RPPEDSTLTTLHDMRYQKLIV
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IPR000198; RhoGAP.
IPR000980; SH2.
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25.7%;
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                                                                                                                                                                                                                                                                                                                                                      PHORBOL-ESTER AND DAG BINDING RHO-GAP.
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                                                                                                                                                                                                                                                                                                                     Score 293.5;
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entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bojesen S.E., Link C., Borkhardt A.; "Genomic structure of the human GRAF gene."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Placenta, Heart, and Liver;
Xia J.H., Tang X.X., Yu K.P., Pan Q., Dai H.P.,
"Molecular cloning of human oligophrenin-1 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Oligophrenin-1 like protein (GTPase regulator associated with focal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98403880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borkhardt A., Bojesen S., Haas O.A., Fuchs U., Ba
Loncarevic I.F., Bohle R.M., Harbott J., Repp R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2), DISEASE, MEDILINE=20381355; PubMed=10908648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from become for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE OF 62-814 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: GTPase activating protein for RhoA.
SUBUNIT: Binds to the C-terminal of pp125(FAK).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and
produced by alternative splicing.
DISEASE: A form of juvenile myelomonocytic leukemia
characterized by a chromosomal translocation t(5;11)
involves OPHNIL and MLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 PH DOMAIN. SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mann S., Henn T., Korth P., Scharr D., Lampert F.;
p human GRAF gene is fused to MLL in a unique t(5;11)(q31;q23)
p alleles are disrupted in three cases of myelodysplastic irome/acute myeloid leukemia with a deletion 5q.";
p. Natl. Acad. Sci. U.S.A. 97:9168-9173(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X. -I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9734811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND VARIANT
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Matches 152
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DOMAIN 265
DOMAIN 390
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DOMAIN 584
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Prodom; PD000066; SH3; 1.
SMART; SM00233; PH; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00326; SH3; 1.
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Pfam; PF00169;
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PS50002; SH3; 1.
                              YC-GILEKH---
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814 AA;
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                                                                                                                                                                                                                                                                                                                           355
92234 MW;
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                      -LNLSSKKK----ESQLQEADSQVDLVRQHFYEVSLEYVFKVQEVQERK
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                                                                                                                                                                                                                                                                                                                   SER RICH.
MISSING (IN ISOFORM 2).
N -> S (IN LEUKEMIA).
/FIId=VAR_013623.
E -> G (IN REF. 2 AND 3).
FC81DBDECB32B18A CRC64;
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                                                                                                                                                                                                                                          Score 290.5;
Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocation;
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                               .5e-11;
                                                                                                                                                                                                                                                                   DB 1;
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ABR_HUMAN
     PRESENTATION OF THE PRESEN
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                                                                                                                                                                                                                                                                                                                                     Tan E.-C., Leung T., Manser E., Lim L.;
"The human active breakpoint cluster region-related gene encodes brain protein with homology to guanine nucleotide exchange protein and GTPase-activating proteins.";
J. Biol. Chem. 268:27291-27298(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR_HUMAN
Q12979; Q1
                                                                                                                                      Heisterkamp N., Kaartinen V., van Soest S., "Human ABR encodes a protein with GAPrac act DBL nucleotide exchange factor domain."; J. Biol. Chem. 268:16903-16906(1993).
  Nucleic Acids
                      Heisterkamp N., Morris C., Groffen "ABR, an active BCR-related gene.",
                                                                    SEQUENCE OF 436-597 FROM MEDLINE-90067847; PubMed-
                                                                                                                                                                                                                                            TISSUE=Fibroblast; MEDLINE=93352461; PubMed=8349582;
                                                                                                                                                                                                                                                                                            SEQUENCE OF 39-859 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Hippocampus;
MEDLINE=94086546; PubMed=8262969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR_HUMAN STANDARD; PRT; 8

2(12)979; Q13693; Q13694;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence up

15-JUN-2002 (Rel. 41, Last annotation

15-JUN-2002 (Rel. 41, Last annotation

Active breakpoint cluster region-relat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQSTE--KQEQRNSIINSSLESVSSNPNSILN--SSSSLQPNMNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAVGELPQANRDTLAFLMIHLQRVAQS-PHTKMDVANLAKVFGPTIVAHAVPNPDPVTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEG----TAQLDSIGFSIIRKCIHAVETRGINEQGLYRIVGVNSRVQKLLSVLMDPKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDIKRQPKVVERLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SETETDICAEWEIKTITSALKTYLRMLPGPLMMYQFQRSFIKAAKLENQESRVSEIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FCFDVEAVDRPGVITMQALSEEDRRLWMEAMDGREPVYNSNKD------SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDFVSKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKI 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLYKTFKLKKRE---KRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDIKFQNIVIEILIENHEKIFNTVPDMPLTN-AQLHLSRKKSSDSKPPSCSERPLTLFHT
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Res. 17:8821-8831(1989).
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                                                                    97 FROM N.A.
PubMed=2587217;
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                                                                                                                                                                                                                                                                                               (LONG
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                                                                                                                                                                                                                                                                                               SHORT
                                                                                                                                                                                            S., Bokoch G.M., Groffe
activity and homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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Best Local (
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SMART; SM00239; PH; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; RhoGEF; 1.
                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                              Guanine-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                            PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSION IN HEART, LUNG AND MUSCLE.
SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (C
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 C2 DOMAIN.
SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
SIMILARITY: STRONG, TO HUMAN BCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOSHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: HIGHLY ENRICHED IN THE BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION:
                                          418
                                                                                                                                                                                                                                                                                                                                                                                                          PF00620;
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L19704;
L19705;
  478
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                     164
                                                                108
                                                                                    374
                                                                                                        48
                                                                                                                              140;
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                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIION: GTPASE-ACTIVATING PROTEIN FOR RAC AND CDC42.
EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP, THEREBY
                                                                                                                                                                                                                                                                                                                         PS500741;
  s-
                   SLDWDSSLVKTFKLKKREKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTV
                                         LLLNSPTIPFRIHNRNGKSYLFLLSSDYERSEWREAIQKLQKKDLQAFVLSSVELQVLTG
                                                      MCDTSGSIQLSEEQKSALAFL----NRGQPSSSNAGNKRLSTIDESGSILSDISFDKTDE
                                                                                    DHEL - - - EDMKMK ISALKSEI ·
                                                                                                      DHELGKYKDLLMKAETERSALDVKLKHARNQVDVETKRRQRAEADCEKLERQIQLTREML
                                                                                                                                                                                                                                                                                                                                             PS50010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000008;
IPR001331;
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IPR000219; |
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657
761
859 AA;
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                                                                                                                                                                                                                                                 91
301
463
463
417
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          ; RhoGAP;
; RhoGEF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC50063.1; -.
AAC37519.1; -.
AAC37518.1; ALT_INIT.
--CFKLRTVHNIPVTSNKDDDESPGLYGFLHVIVHSAKGFKQSANLYCTLEV
                                                                                                                                                                                                                                                                                                                        PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                 DH_1;
                                                                                                                                                                   67
660
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97696
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595
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                                                                                                                                       8.7%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PΗ
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                                                                                                                                                               POLY-LEU.

MEPLSHRGLERLSWIDTLYSNESYGTDEYDGEGNEBOKGPP
EGSETMPYIDESPTMSPOLSARSOGRGDGVSPTPPEGLAPG
-> MEEEEEALGLLDKYLEDEDVYLLEECELGTPTSPGSGS
PFLYAVK (IN SHORT ISOFORM).

R -> G (IN REF. 2).
R SKV -> VGGA (IN REF. 2).
L -> V (IN REF. 2).
L -> V (IN REF. 2).
                                                                                                                              67;
                                                                                                                            Score 282; DB 1;
Pred. No. 1.7e-10;
7; Mismatches 201;
                                                                                                                                                                                                                                                                             PH.
C2 DOMAIN.
                                                                                                                                                                                                                                                                                                  factor; Alternative DH.
                                                                                                                                                                                                                                                                    RHO-GAP
                                                                                   -----QKEKANKGQSRA---IERLKKKM-FENEFL
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RESULT 12
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DT 01-FEB
DT 0
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01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Iatreille P., Lightning J., Lloyd C., Mortinore B., O'Callaghan I
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R
Sulston J., Thierry-Mieg J., Thomas K., Vaudhan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Sins ... Sulston J., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YN54_CAEEL P34588;
                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                 elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                   "2.2 Mb of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                             -!- SIMILARITY:
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                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
     L16685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIHLQRVAQ-SPHTKMDVANLAKVFGPTIV-----AHAVPNPDPVTMSQDIKRQPKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEHLKRVAEKEPINKMSLHNLATVFGPTLLRPSEVESKAHLTSAAD - - IWSHDVMAQVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIAGTLKLYFRELPEPLLTDRLYPAFMEGIALSDPAAKENCMMHLLRSLPDPNLITFLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFL
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                                                                                                                                                                                                                                                                                                                                                                                           contiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
1 protein ZC21.4 in chromosome III
        AAA28171.1;
1RGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                             CONTAINS 1 RHO-GAP DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Α.,
                                                                                                                                                                                                                                                                                                                                                                                                nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weinstock L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilkinson-Sproat
                                                                                                                                                                                                      There are no
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                                                                                                                                         Usage
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                                                                                                                                                                                                   restrictions
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RESULT 13
BCR_HUMAN
ID BCR_HOMAN
ID BCR_HOMAN
ID BCR_HOMAN
ID 101-JU
DT 01-JU
DT 15-JU
DT 11-JU
DT 11-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHUMAN STANDARD,
P11274; Q12842;
P11274; Q12842;
O1-JUL-1989 (Rel. 11, Created)
T 01-JUL-1989 (Rel. 11, Last sequence updated)
T 15-JUN-2002 (Rel. 41, Last annotation updated)
T 15-JUN-2002 (Rel. 41, Last annotation updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          area, Primare BCR OR BCR1.

Homo sapiens (Human).

Homo sapiens (Human).

Horia; Metazoa; Chordata;

Horia; Primates;
                                                                   "cDNA sequence for human bcr, the gene oncogene in chronic myeloid leukaemia. EMBO J. 6:115-119(1987).
                                                                                                                                                                                                                                                                                                                                    Chissoe S.L., Bodenteich A., Wang Y.-F., Wan Clifton S.W., Crabtree J., Freeman A., Iyer McLaury H.-J., Pan H.-Q., Sarhan O.H., Toth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM003;
Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=95394474; PubMed=7665185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00620; RhoGAP; 1. SMART; SM00324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormPep; 2C21.4; CE00534
InterPro; IPR000198; Rho
                           SEQUENCE
                                                                                                                                                                                              SEQUENCE OF 1-872 FROM N.A.
                                                                                                                                                                                                                                              Genomics 27:67-82(1995).
                                                                                                                                                                                                                                                                  Heisterkamp N., Groffen J., Roe B.A.; "Sequence and analysis of the human A regions involved in the Philadelphia
     MEDLINE=85240564;
                                                                                                                                                                     MEDLINE=87218455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNPDPV-TMSQDIKRQPKVVERLLSLPLEYWSQFMMVEQENIDPLHVIENSNAFSTPQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --FLRVKTVPLLSKVD------DIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMRLHDFVSKTVIKPESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IENGEAPTATATTPKSGRKWKKSKAAKQGSGGSSGSSGSSGSQQ-----QGAAGAPQPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPNDGGPIEAVSTIETVPYWTRSRRKTGTLQPWNSDSTLNSRQLEPRTETDSVGTPQSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSDDNMATMVTHMSDQCKIIETLIHYNLWMFDESSTTE-DAVPEQHPADGQN----PLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHNRLHKLRNLLRKLPRPHYDTLRFLIVHLSEITKHSDVNKMECRNLALMFGPSIVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANLAKVFGPTIVAHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGFDSVD----LSKVESLDPRWRDVNVVSSLLKMFLRKLPEPLLTDKLYPFFIDANRIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVKIGEGMLADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEK---
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747 AA; 8
                              683-1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DIKVSLLGPVTTPEHQLLKTPSSSSLS---
                                                                                                                                                                     PubMed=3107980;
     71 FROM N.A.
PubMed=2989703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80829 MW;
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25.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 280.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48E9D61EDC4C56B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 1.7e-10;
                                                                                                                                                                                                                                                                                         ABL gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1271
                                                                                                                                                                                                                                                                  chromosomal translocation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
2.7.1.-).
                                                                                                                        that translocates
                                                                                                                                                                                                                                                                                                                    ver K., \hat{h} S., W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146;
                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                      Y.-P.,
                                                                                                                                                                                                                                                                                                                                         Jian
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QRVRSTLTKNTPRFGSKSK 614
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                                                                                                                                                                                                                                                                                                                                    Burian D.,
L., Ma Y.,
Z., Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCEDH---
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BINDING TO ABL SH2-DOMAIN.
BINDING TO ABL SH2-DOMAIN.
MEDLINE-91300547; PubMed-1712671;
Pendergast A.M., Muller A.J., Havilk M.H., Maru Y., Witte O.N.;
Pendergast A.M., Muller A.J., Havilk M.H., Maru Y., Witte O.N.;
"BCR sequences essential for transformation by the BCR-ABL oncogene
"BCR sequences essential for transformation by the BCR-ABL oncogene
"BCR sequences essential for transformation by the BCR-ABL oncogene
                                                                                                                                                                  "The BCR gene encodes a a single exon."; Cell 67:459-468(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91172169; PubMed-1900918; Shah N.P., Witte O.N., Denny C.T.; "Characterization of the BCR promoter positive and "negative cell lines."; Mol. Cell. Biol. 11:1854-1860(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87092329; PubMed=3540951; Mes-Masson A.M., McLaughlin J., Daley G.Q., Paskind M., Wit Mes-Masson Pallorable follower define the complete coding region P210c-abl gene product associated with chronic myelogenous cells containing the Philadelphia chromosome."; Proc. Natl. Acad. Sci. U.S.A. 83:9768-9772(1986).
                                                                                                                                                                                                                                                                                                                                                           dependent manner.";
Cell 66:161-171(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91238969; PubMed-1903516;
Diekman D., Brill S., Garrett M.D.,
Monfries C., Hall C., Lim L., Hall A.
"Bcr encodes a GTPase-activating prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fainstein E., marci
Fainst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhu Q.S., Heisterkamp N., Groffen J.;
"Unique organization of the human BCR
Nucleic Acids Res. 18:7119-7125(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lifshitz B., Fainstein E., Ma
Gale R.P., Canaani E.;
"bcr genes and transcripts.";
Oncogene 2:113-117(1988).
                                                                                            +
                                                                                                                                                                                                                                                                                     MEDLINE=92034969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88065859; PubMed=2825022; Fainstein E., Marcelle C., Rosner A., Dreazen O., Smith S.D., Croce C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91088292;
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Nature 315:758-761(1985).
                                                                                                                                                                                                                                                            Maru Y., Witte O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 351:400-402(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A new fused transcript in lymphocytic leukaemia.";
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                 THEM. DISPLAYS SERINE/THREONINE KINASE ACTIVITY.

DOMAIN: THE REGION INVOLVED IN BINDING TO ABL SH2-DOMAIN IS

DOMAIN: THE REGION INVOLVED IN BESERYTHR PHOSPHORYLATED PH

SH2 BINDING. THIS REGION IS ESSENTIAL FOR THE ACTIVATION OF

ABL TYROSINE KINASE AND TRANSFORMING POTENTIAL OF THE CHIMBH
                                                                                                                                       FUNCTION: GTPASE-ACTIVATING PROTEIN FOR RAC1 ATHE EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP,
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                                                                                                                                                                                                                                                                                        PubMed=1657398;
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stein E., Marcelle
REGION IS ESSE...
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                    OSPHORYLATED PRIOR ACTIVATION OF THE L OF THE CHIMERIC
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BCR-ABL ONCOGENE

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         Pfam; PF00620; RhogAP; 1.
Pfam; PF00621; RhogEF; 1.
SMART; SM00239; C2; 1.
SMART; SM00239; C2; 1.
SMART; SM00234; RhogAP; 1.
SMART; SM00325; RhogEF; 1.
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EMBL;
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                                                                                                                                                                                                                                               PROSITE; PS50004; C2_DOMAIN_;
PROSITE; PS50010; DH_2; 1.
PROSITE; PS00741; DH_1; 1.
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                SEQUENCE
                                                                        CONFLICT
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                                                                                                                                                                                                                            Chromosomal translocation;
                                                                                                                                                                                                                                     Guanine-nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute lymphoblastic leukemia (ALL).
SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 C2 DOMAIN.
SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
SIMILARITY: STRONG, TO HUMAN ABR AND DROSOPHILA ROTUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: AUTOPHOSPHORYLATED.

DISEASE: Participates in a t(9;22)(q34;q11) chromosomal translocation that produces a BCR-ABL oncogene responsible chronic myeloid leukemia (CML), acute myeloid leukemia (AML)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;; U07000; AAB60388.1; -.; M24603; AAA65939.1; -.; Y00661; CAA68676.1; -.; X002996; CAA26441.1; -.; M15025; AAA35594.1; -.
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                                                                                                                                                                                                                                                                                                                                                         PF00168;
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M64437; -; NOT_ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:1014; BCR.
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M00325; RhoGEF; 1.
PS50004; C2_DOMAIN_2;
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IPR000198;
IPR000219;
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IPR001331; GDS_CDC24.
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RhoGAP.
8.5%;
24.0%;
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                         BREAKPOINT FOR TRANSLOCATION TO
BREAKPOINT FOR TRANSLOCATION TO
BCR-ABL ONCOGENE.
M -> I (IN REF. 4).
G -> D (IN REF. 4).
E -> K (IN REF. 4).
E -> D (IN REF. 4).
S -> N (IN REF. 1).
MISSING (IN REF. 4).
 Score
Pred.
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factor; Proto-oncogene;
                                                                                                                                       POLY-LEU
                                                                                                                                                                       DOMAIN.
275.5; DB 1;
No. 7.5e-10;
                                                                                                                                                  SH2-DOMAIN
          Length
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PubMed=10818214;
Billuart P., Chelly J., Carrie A., Vinet M.C., Couvert P.,
McDonell N., Zemni R., Kahn A., Moraine C., Beldjord C., Bier
"Determination of the gene structure of human oligophrenin-1
                                                                                                                                Billuart P., Bienvenu T., Ronce N., Zemni R., Roest Crollius H., Carrie Brillaut S., Hamel B., Fryns J.-P.,
                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                     060890; Q8WX47;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                         _HUMAN
                                                                                                                     Brillaut S., Chelly J.;
                                                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=98241228; PubMed=9582072;
                                                                                                                                                                                                                                                                                                                                                          OPH1_HUMAN
                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                 OPHN1
                                                                                                                                                                                                                                                                                          Oligophrenin
                                                                                 Nature 392:923-926(1998).
                                                                                                retardation."
                                                                                                          "Oligophrenin-1
                                                                                                                                                                                                    SEQUENCE FROM N.A.,
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Metazoa; Chordata; C
Metazoa; Primates; (
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                                                        AND VARIANTS
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Beldjord C., Ka
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F., Cherry
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                 Bienvenu
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Best Local :
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                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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164 patients with non-specific X-linked mental retardation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family. Could activates GTP hydrolysis of members of the family. Could activates GTPase targets that are know cell migration and outgrowth of axons and dendrites. TISSUE SPECIFICITY: Expressed in brain.

DISEASE: Defects in Ophul are the cause of X-linked mental retardation (XLMR) type 60 (MRX60).

SIMILARITY: CONTAINS 1 PH NOMBATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a copyright is produced through a copyright institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mental retardation (XLMR) type 60 (MRX SIMILARITY: CONTAINS 1 PH DOMAIN. SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
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AJ248261
AJ248262
AJ248263
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AJ248251;
AJ248252;
AJ248253;
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AJ248257;
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AJ248259;
                          164;
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AJ248245;
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    12
                                                                                                                                                                                                                        PF00169; PH;
                                                                                                                                                                                        SM00324;
                                                                                                                                                                 activation;
                                                                                                                                                                                                                                                                     HGNC:8148;
                                     Similarity
  FEQLVRRV--
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                          Conservative
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22.2%;
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20; Mismatches
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JOINED
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PRO-RICH.
A -> T.
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T -> M
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A24D150048071608
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                                     6e-09;
  -QFIQLAKDFE-DFRKKWQRTDHELG-
                                               DB
                          249;
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16-OCT-2001 (Rel. 40, I
15-JUN-2002 (Rel. 41, I
Rho-GTPase-activating F
STRAIN=129/Sv;

MEDLINB-20164286; PubMed-10699171;

Prakash S.K., Paylor R., Jenna S.,

Xu B., Mancini M.A., Zoghbi H.Y.;

"Functional analysis of ARHGAP6; a
                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                               054834; Q9QZL8
                                                         SEQUENCE FROM N.A.,
                                                                                                                  Mus musculus (Mouse)
                                                                                                                                        RhoGAPX-1).
                                                                                                                                                                                                             RHG6_MOUSE
                                                                                                                               ARHGAP6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TMTPMEQKP-
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                                                                                                                                                                                                             STANDARD;
                                                                                            Chordata;
Rodentia;
                                                          REVISIONS
                                                                                                                                                  Last sequence update)
Last annotation update)
protein 6 (Rho-type GTPase-activating
                                                                                                                                                                                      Created)
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Sciurognathi;
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  novel
                         Lamarche-Vane
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  GTPase-activating
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EMBL; AF177664; AAD55086.1; --
HSSP; Q07960; 1RGP;
MGD; MGI:1196332; Arhgap6.
InterPro; IPR000198; RhoGAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schaefer L., Prakash S.K., Zoghbi H.Y.;
"Cloning and characterization of a novel rho-type GTPase-activating protein gene (ARHGAP6) from the critical region for microphthalmia with linear skin defects.";
Genomics 46:268-277(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative splicing; GTPase SITE 343 353 DOMAIN 412 573
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (Potential).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: GTPASE ACTIVATOR FOR THE RHO-TYPE GTPASES BY CONVERTING THEM TO AN INACTIVE GDP-BOUND STATE. COULD REGULATE THE INTERACTIONS OF SIGNALING MOLECULES WITH THE ACTIN CYTOSKELETON. PROMOTES CONTINUOUS ELONGATION OF CYTOPLASMIC PROCESSES DURING CELL MOTILITY AND SIMULTANEOUS RETRACTION OF THE CELL BODY CHANGING THE CELL MORPHOLOGY (BY SIMILARITY).
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                        PMIPSIVVHCVNEIEQRGLTETGLXRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAIC
                                                                                                                                                AFLNRGQPSSSNAGNKRLSTIDES-GSILSDISFDKTDESLDWDSSLVKTFKLK---KRE 181
                                                               SLPAEAQSK----KEKARDKKLSLNPIYR-
                                                                                                                                                                                              EQKDASSDFVSSLLPFGNKKQNKELSSS----NSSL--SSTSETPNES---TSPNTPEPA
                                                                                                                                                                                                                            KRRSTSRQFVDG--PPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETV 239
                                                                                                                                                                                                                                                              KSLRKNLDSLGKEKNKDKEFIPQAFGMPLSQVIAND-----RAYKLKQDLQRE
                                                                                                                                                                                                                                                                                                                                                              SALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEEQKSAL 125
-QVPRLVDSCCQHLEKHGLQTVGIFRVGSSKKRVRQLREEFDRGVDV-CLEEEHSVHDVA 467
                                                                                            CVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPCIPTLIGTPVKIGEGMLADFVSQTS 359
                                                                                                                             P---RARRR-GAM-----SVDSI-----TDLDDNQSRLLEALQL
                                                                                                                                                                                                                                                                                                                              SGRSVRLRSVPIQSLSELERARLQEVAFYQLQQD------CDLGCQITIPKDGQKRK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genet. 9:477-488(2000).
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PASDFTP (IN ISOFORM 2).

108786 MISSING (IN ISOFORM 2).

108786 MW; 40800B6457D34CE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 93; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 251.5; DB 1
Pred. No. 1.8e-08;
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SH3-BINDING.
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                                                                                                                                                                                              ALLKEFLROMPOPULTRELYTAFINTL-LLEPEEQLGTLQLLIYLLPPCNCDTLHRLLQF
RKASQSSSPD--ILQTEVSFSMGGRHSST
                                                              TAIIAVVQKMI--
                              ---GPVTTPEHQLLKTPSSSSLSQRVRST
                                                                                                                                                             LQRVAQSPH-----
                                                                                         -----VYERLLSLPLEYWSQFMMVEQENIDPLHVI----ENSNAFSTPQT-PDIKVSLL- 575
                                                                                                                             LSIVARHADDNVSKDGQEVTGNKMTSLNLATIFGPNLL-HKQKSSDKEYSVQSSARAEES
                                                                                                                                                          ----TKMDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPK- 526
                                                             ENYDSLEMVPPDLQNEVLISLLETDPDVVDYLLR
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Search completed: July 3, 2003, 09:54:41
Job time: 28 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            : /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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US-09-764-868-878
US-10-080-960-32
US-09-764-868-898
US-10-132-585-5
US-10-132-585-5
US-09-764-868-1029
US-09-764-868-1029
US-09-764-868-1024
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0 US-09-833-790-413

0 US-09-833-790-427

0 US-09-881-736-4

0 US-09-881-736-6

0 US-09-881-736-6

0 US-09-802-127-8

US-10-153-668-470
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                                           Sequence 4, Appli
Sequence 6, Appli
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Sequence 17, Appli
Sequence 878, Appli
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Sequence 2, Appli
Sequence 1024, Ap
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Sequence
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Sequence 413, App
Sequence 427, App
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## ALIGNMENTS

US-09-881-736-2

GENERAL INFORMATION:

Jantsch-Plunger, Verena

Sequence 2, Application US/09881736 Patent No. US20020076785A1

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PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: To be determined
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 632
TYPE: PRT
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CURRENT FILING DATE: 2001-06:18
PRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR FILING DATE: 2000-06:19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glotzer, Michael
APPLICANT: Jantsch-Plunger
APPLICANT: Romano, Alper
APPLICANT: Mishima, Masano
APPLICANT: Kaitna, Susanne
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APPLICANT: Mishima, Masanori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use
TITLE OF INVENTION: Screening methods
TITLE OF INVENTION: Screening methods
TITLE OF INVENTION: Screening methods
                                                                                                                                                                                  Local
                                                                                                                                                              tch 100.0%; Score 3243; DB 10; al Similarity 100.0%; Pred. No. 2.7e-239; 632; Conservative 0; Mismatches 0;
61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE
                     61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQLSEE
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APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
                                                                                                  Query Match
Best Local S
Matches 630
                                                                                                                                                                                     SEQ ID NO 413
LENGTH: 632
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                           TYPE: PRT
                                                                                                  Local Similarity hes 630; Conserv
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                                                            MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELGKYKDLLMK
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Indirias, Carol Y.
                                                                                                  Conservative
                                                                                                            99.6%;
                                                                                                Score 3230; DB 10;
Pred. No. 2.6e-238;
0; Mismatches 2;
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                                                                                                                                            APPLICANT: Indirias, Carol Y.

APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 427
LENGTH: 570
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-833-790-427
; Sequence 427, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 569; Conserv
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APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
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TERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMIMCDTSGSIQLSEEQK
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                                                                                                  Conservative
                                                                                                            90.0%;
                                                                                                 0;
                                                                                                            Score 2919; DB 10;
Pred. No. 1.3e-214;
                                                                                                  Mismatches
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Sequence 4, Application US/09881736

Patent No. US20020076785A1

GENERAL INFORMATION:

APPLICANT: Glotzer, Michael

APPLICANT: Jantsch-Plunger, Verena

APPLICANT: Kaitna, Masanori

APPLICANT: Kaitna, Susanne

TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in

TITLE OF INVENTION: Screening methods

FILE REFERENCE: 0652.2260001/EKS/AES

CURRENT APPLICATION NUMBER: US/09/881,736

CURRENT APPLICATION NUMBER: EP 00 112 880.0

PRIOR APPLICATION NUMBER: EP 00 112 880.0

PRIOR APPLICATION NUMBER: EP 01 110 554.1

PRIOR FILING DATE: 2000-04-30

PRIOR APPLICATION NUMBER: 60/241,231

PRIOR APPLICATION NUMBER: To be determined

PRIOR FILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 6

SOFTMARE: Patentin Ver. 2.1
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; LENGTH: 628
; TYPE: PRT
; ORCANISM: Mus musculus
US-09-881-736-4
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                                                                                                                    Conservative
                                                                                                                                   84.3%; Score 2734; DB 10; 84.4%; Pred. No. 2e-200;
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                                          ; LENGTH: 681
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-881-736-6
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US-09-881-736-6
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Query Match
                                                                                                                                       SEQ ID NO 6
                                                                                                                                                                                                                                              APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their
TITLE OF INVENTION: Screening methods
FILE REFERENCE: 0652.2260001/EKS/AES
CURRENT EFFERCE: 0652.2260001/EKS/AES
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: EP 01 110 554.1
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020076785A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09881736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Glotzer, Michael
APPLICANT: Jantsch-Plunger,
APPLICANT: Romano, Alper
APPLICANT: Mishima, Masanon
APPLICANT: Kaitna, Susanne
                                                                                                                                                                         PRIOR APPLICATION NUMBER: To be PRIOR FILING DATE: 2001-06-13 NUMBER OF SEC ID NOS: 6
                                                                                                                                                          SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540
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Mishima, Masanori
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16.7%;
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41; 193;

Gaps

----TDE 451

172

57

413 8

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GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Meyers, Rachel

TITLE OF INVENTION: No. US20020045212Alel Human GTPase Activator Proteins
FILE REFERENCE: 035800/158994

CURRENT APPLICATION NUMBER: US/09/802,127

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 60/185,611

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 193
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09802127 Patent No. US20020045212A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          SULT 6
-09-802-127-8
                            ORGANISM: Artificial Sequence FEATURE:
       OTHER INFORMATION:
                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRDTLAYLFIHWRKVIAQSSRNKMNCEAMARMVAPAVMGH-----PVKQSQSQAIAGRD 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRDTLAFLMIHLQRV-AQSPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMSQ-----D 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LHDVEVITDTLKRFLRDLKDPLIPRTSRQELIVAANLYSTDPDNGRLALNRVICELPQA
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       Rho-Gap3 consensus
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109; Mismatches 285;
  sequence
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; ORGANISM: HOMO
US-10-153-668-212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 212
LENGTH: 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 212, Application US/10153668 Publication No. US20030092616A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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APPLICANT: MATSUDA, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STATE Activating Gene
FILE REFERENCE: 1254-0207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/316,031 PRIOR FILING DATE: 2001-08-31 PRIOR APPLICATION NUMBER: US 60/328,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/153,668 CURRENT FILING DATE: 2002-05-24 PRIOR APPLICATION NUMBER: US 60/293,172 PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
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APPLICANT: MATSUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 2001-313175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-08-30
                                               307
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                                               QTTPSEEEQPISVNA
                                                                                                                                      GSRKDSSSEVFSDAAKEGWLHFRPLVTDKGKRVGGSIRPWKQMYVVLRGHSLYLYKDKRE
                                                                                                                                                                                                                               DHESYGPPSLDAQPNSKTERSKSYDEGLDDYREDAKLSFKHVSSLKGIKIADSQKSSEDS
                                                                                                                                                                                                                                                              DHE-LGKYK-DLLMKAETERSAL------DVKL--KHARNQVDVEIKRRQRAEADC
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  DESIDWDSSLVKTFKLKKREKRRSTSRQFVDGPPGPVKKTRSIGSAVDQGNESIVAKTTV
                                                                                         ALAFLNRGQPSSSNAGNKRLSTIDESGSILSDISFDKT----
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                                                                                                                                                                                                                                                                                                                       8.8%; Score 286.5; DB 9;
22.1%; Pred. No. 4.8e-13;
tive 98; Mismatches 216;
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Pred. No. 7.5e-15;
26; Mismatches 54;
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                                               --CLIDISYSETKRKNVFRLTTSDCECLFQAEDR
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US-10-153-668-470
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                                                                                                                                                                                                 SOFTWARE: PatentIn
SEQ ID NO 470
LENGTH: 1354
                                                                          Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/153,668 CURRENT FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
                                                                                                                                                                                                                                  PRIOR FILING FILE NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/293,172 PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MATSUDA, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HONDA,
                                                                                                                                                                                  LENGTH:
TYPE: PI
                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-10-10
                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 2001-157043
FILING DATE: 2001-05-25
APPLICATION NUMBER: JP 2001-260681
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 2001-313175
                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-08-30
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                                 48 DHE-LGKYK-DLLMKAETERSAL------DVKL--KHARNQVDVEIKRRQRAEADC
                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDMLAWIKTIQESSNLNE-EDTGVTNRDLIS---RRIKEYNNLMSKAEQ-----LPKT--
DHESVGPPSLDAQPNSKTERSKSYDEGLDDYREDAKLSFKHVSSLKGIKIADSQKSSEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDIKVSLLGPVTTPEHQLLKT----PSSSSLSQRVRSTLTKNTPRFGS 611
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                                                                          Conservative
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                                                                                         8.8%;
22.1%;
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                                                                  ; 86
                                                                 Score 286.5; DB y;
Pred. No. 5.2e-13;
                                                                                                         Length 1354;
                                                                      Indels
                                                                      191;
                                                                      Gaps
 314
                                     93
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US-09-851-682A-1

TYPE: PRT ORGANISM: Homo sapien

Query Match

Matches 130; Best Local Similarity

Conservative

75;

Mismatches 20

203;

Indels 125; Length 2548;

Gaps

24;

8.3%; Score 270.5; DB 10; 24.4%; Pred. No. 2.2e-11;

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RESULT 9
US-09-851-682A-1
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SEQ ID NO 1
LENGTH: 2548
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09851682A Patent No. US20020091248A1
                                                        PRIOR APPLICATION NUMBER: US/09/172,422 PRIOR FILING DATE: 1998-10-14 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                     APPLICANT: Welch, Juliet
TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES,
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREC
                                                                                                                                                                                                                                                                                                                        APPLICANT: Adams, Arwen E. APPLICANT: Chiu, Choi Ying APPLICANT: Duhl, David
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/851,682A CURRENT FILING DATE: 2001-05-08
                                                                                                                                                             FILE REFERENCE: 200130.442
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                                       SOFTWARE: FastSEQ
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Sheffield, Val
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                                       for Windows Version
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US-09-764-868-878
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 878
                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                          LENGTH: 555
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
-09-764-868-878
                                                                                                                                                                                                                                                                           Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
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                                           CRECNSYVYF - - QGAECEECCLACHKKCLETLAIQCGHKKLQGRLQLFGQ - - - - DFSHAA 186
                                                                            CVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPC-IPTLIGTPVKIGEGMLADF--VS
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Sequence 7, Application US/09802127
Patent No. US20020045212A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: No. US20020045212A:
FILE REFERENCE: 035800/158994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 32
LENGTH: 170
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/10/080,960
CURRENT FILING DATE: 2001-10-19
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 ON: NO. US20020045212A1el 035800/158994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 251; DB 9;
Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386
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                         Human
                       GTPase Activator Proteins
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414 -DIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAA--EITDEDNSIAAMYQAV-GELPQAN 469
                                                                                                                                          363 PSIVVHCVNEIE------QRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVD----
FDVHVVAGLLKLYLRELPEPLIPYDLYEEFIRAAKEQIEDPDERLRALKELLSSKLPRAH
                                                                                                         PIIVEKCVEYIEKLYPLAERGLQEEGIYRVSGSASRVKELREAFDKDGAPDSLELSEKEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----MYQAVGELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANLAKVFGPTIVAHAVPNP 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDISNVLKLYLRQLPEPLISFRLYHELVGLAKDSLKAEAEAKAASRGRQDGSESEAVAVA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF HUMAN PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                              Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-764-868-898
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US-09-764-868-898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 898
LENGTH: 291
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 898, Application US/09764868
Patent NO. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/802,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185,611
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 PSIVVHCVNEIE-----QRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVD---
                                                                                                                                                                                                                                                                                                                                                                              263 SRQLEPRTETDSVGTPQ-----SNGGMRLHDFVSKTVIKPE--SCVPCGKRIKFGKLSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YNTLRYLLTHLNRVAEIYIENSAVNKMNARNLAIVFGPTLL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 -DIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAA--EITDEDNSIAAMYQAV-GELPQAN 469
                                                                                                                                                                                                                                                      58
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                                                                                                                                                                                                                                                                                                                                     1 SRSLDSPTSSPGAGTRQLVKASSTGTESSDDFEER---DPDLGDGLENGLGSPFGKWTLS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PIIVEKCVEYIEKLYPLAERGLQEEGIYRVSGSASRVKELREAFDKDGAPDSLELSEKEW
PSPEVIRSLKTLLVQLPDSNYNTLRHLVAHLFRVAARFMENKMSANNLGIVFGPTLL 288
                                                                                                                                                                                                    KIGEGML---ADFVSQTSPMIPSIVVHCVNEIEQRGLTETGLYRISGCDRTVKELKEKFL 401
                                                                                                                                                                                                                                                    SAAQTHQLRRLRGPAKCRECEAFMVSGTECEECFLTCHKRCLETLLILCGHRRLPARTPL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDTLAFLMIHLQRVAQ-----SPHTKMDVANLAKVFGPTIV 505
                                     ---NSIAAMYQAVGELPQANRDTLAFLMIHLQRV-AQSPHTKMDVANLAKVFGPTIV 505
                                                                                NGRALVELSG-NSPHDVSSVLKRFLQELTEPVIPFHLYDAFISLAKTLHADPGDDPGTPS 231
                                                                                                                     RVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDED------
                                                                                                                                                                 -FGVDFLQLPRDFPEE----VPFVVTKCTAEIEHRALDVQGIYRVSGSRVRVERLCQAFE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDVHVVAGLLKLYLRELPEPLIPYDLYEEFIRAAKEQIEDPDERLRALKELLSSKLPRAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 247.5; DB 9; 30.0%; Pred. No. 5.3e-11;
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Pred. No. 1.3e-11;
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US-10-080-960-34
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US-10-132-585-5
; OTHER INFORMATION: Consensus amino acid sequence US-10-080-960-34
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/242,040
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,992
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,637
PRIOR APPLICATION NUMBER: US 60/242,637
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosanna
TITLE OF INVENTION: 26030, A HUMAN RHO-GAP FAMILY MEMBER AND
TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/10080960 Publication No. US20020197695A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10132585 Publication No. US20030055234A1
                                                                                                                               SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 80090, 52874,52880,63497,
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 38155-20044.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: MPIO1-101P1RM
CURRENT APPLICATION NUMBER: US/10/132,585
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,581
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-10-19
                                                                                                                                                      SOFTWARE: FastSEQ
                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 152
TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: ProDom consensus rhoGAP domain
                                           FEATURE:
                                                                                                           ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 ELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANLAKVFGPTIVAHAVPNP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 LSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEA--AEITDEDNSIAA---MYQAVG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 MEEYEDVHTVAGLLKQYFRELPEPLLTYELYEEFIEAAKAQVSDEDERMEALEMLKELIK 70
                                                                                                           103
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                                                                                                                                                      Windows Version
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Pred. No. 1.
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hes 39;
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Best Match	Utery Match 6.7%; Score 218; DB 9; Length 103; Best Local Similarity 45.1%; Pred. No. 2.1e-09; Matches 46; Conservative 21; Mismatches 29; Indels 6; Gaps 3;
Qy	409 LSKVDDIHAICSLLKDFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVG 463
Дb	2 MEEYEDVHTVAGLLKQYFRELPEPLLTYELYEEFIEAAKAQVSDEDERMEALEMLKELIK 61
Qy	464 ELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANLAKVFGPTI 504
<b>B</b>	62 LLPEANRETLRYLLKHISRVAQHSEENKMNAQNLAVVFGPTL 103
Search Job tim	Search completed: July 3, 2003, 10:05:54 Job time : 57 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                       191
183.5
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297 PESCVPCGKRIKFGKLSLKCRDCRVVSHPECRDRCPLPC----IP---TLIGTPVKIGEG

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483 NKHLNSSQPSGFGPANSLEDVVRLPDSSNKIEEDRCSNSADIT----GPSFIRSWTFGMFS 539

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т 89	9 R 1 372 R	ät	SULT 1 -09-080-855-2 -09-080-855-2 Sequence 2, Applicat Patent No. 6083721 REPLICANT: SETANS, APPLICANT: STANS, APPLICANT: HAIMEN, APPLICANT: HAIMEN, APPLICANT: HAIMEN, APPLICANT: HOLDING, TITLE OF INVENTION: FILE REFERENCE: L04 REPLICATI FILING DATE EARLIER APPLICATION CURRENT FILING DATE EARLIER FILING EARLIER EARLIER FILING EARLIER EARLIER FILING EARLIER F	•	114 113.5 1113.5 112.5 112.5 112.5 112.5 113.5 113.5 114 111 111 111 111 111 111 111 111 11
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RNQVDVEI	RRVEILSE ::       OKVEE	9.3%; Soy 22.4%; Pirvative 120;	y ation US/090 y Jan Jan Petra rm, Pontus Leonel Jorg Leonel Jorg 1461/7030 NN NUMBER: UP 98-05- NN NUMBER: UP 98-05- NN STRE: 1997-02- NOS: 39 for Windows		894 713 713 942 942 1003 1003 1003 1103 1013 1013 1013 101
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LENGTH: 2548
TYPE: PRT
ORGANISM: Homo sapien
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APPLICANT: Leng, Song
APPLICANT: Leng, Song
APPLICANT: Welch, Juliet
TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, I
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOE
FILE REFERENCE: 200130.442
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SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1e-15;
75; Mismatches 203;
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RESULT 3
PCT-US93-03076-10
                                                                                    ; MOLECULE TYPE: protein PCT-US93-03076-10
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
TITLE OF INVENTION: GAP-Associated Protein p190 and
TITLE OF INVENTION: Transduction
NUMBER OF SEQUENCES: 20
                                         Query Match
                                                                                                                                                                                                                         TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS: LENGTH: 165 amino acids
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                         Local
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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64; Conserv
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19930331
                    7.9%;
; Score 257.5; DB 5;
; Pred. No. 1.8e-16;
33; Mismatches 63;
                                                                                                                                                                                                                                                                                                                  WHI92-03A
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                                           Length 165;
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369 CVNEIEQRGLTETGLYRISGCDRTVKELKEKFLR--VKTVPLLSKVDDIHAICSLLKDFL 426

Indels

9;

Gaps

Conservative

CIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKADISVNMYEDINIITGALKLYF

60

RNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRVAQS 486 RDLPIPLITYDAYPKFIESAKIMDPDEQLETLHEALKLLPPAHCETLRYLMAHLKRV--T

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RESULT 4

PCT-US93-03076-9

Sequence 9, Application PC/TUS9303076

GENERAL INFORMATION:

APPLICANT: Whitehead Institute for INVENTION: GAP-ASSOCIATE

TITLE OF INVENTION: Transduction

TITLE OF INVENTION: 720
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PCT-US93-03076-2
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                                                                                      Sequence 2, Application PC/TUS9303076
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for
TITLE OF INVENTION: GAP-Associated
TITLE OF INVENTION: Transduction
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.#1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03076
FILING DATE: 19930331
CLASSIFICATION:
                                                 NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
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NAME: Granahan, patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                   STREET:
                                 ADDRESSEE:
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Lexington
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                 E: Hamilton, Brook, Smith & Reynolds, P.C.
2 Militia Drive
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2 Militia Drive
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 327
REFERENCE/DOCKET NUMBER: WHI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 19.1%;
les 125; Conservative 9
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02173
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                                                   SHNNKVNLMTSENLSICFWPTLMRPDFSSMDALTATRSYQ---TIIELFIQQCPFFFYNR 1439
                                                                                        AQSPHTK-MDVANLAKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLS---
                                                                                                                                                                 DFLRNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFLMIHLQRV
                                                                                                                                                                                                                                         SIVVHCVNEIEORGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICSLLK
                                                                                                                                                                                                                                                                                   RRRNILRSLRRNTKKPKPK---PRPSITKATWESNYFGVP-----LTTVVTPEKP-IP
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                                                                                                                                                                                                                                                                                                                                                                                               KTVIKPESCVPCGK----RIKF-----GKLSLKCRD-----
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Pred. No. 2.3e-10;
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                                         RESULT 7
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; TYPE: PRT
; ORGANISM: Ashbya gossypii
US-09-415-522-6
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Sequence 8, Application PC/TUS9303076 GENERAL INFORMATION:
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APPLICANT: Wendland, Juergen
APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Peter
APPLICANT: OP INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 6291660 TITLE OF INVENTION: Development FILE REFERENCE: CGC2046
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Pred. No. 2.4e-08;
                                                                                                                                                              -IVAHAVPNPD 513
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US-09-415-522-8
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                      US-09-415-522-8
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                                                                             SEQ ID NO 8
LENGTH: 1013
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                                                                                                                                                                                                                                                                                                                                         Sequence 8, App
Patent No. 6291
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                                                                                                                                                                                                            APPLICANT: Gaffney, Thomas
APPLICANT: Wendland, Juergen
APPLICANT: Philippsen, Peter
TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No.
TITLE OF INVENTION: Development
                                                                                                                                                        FILE REFERENCE: CGC2046
CURRENT APPLICATION NUMBER: US/09/415,522A
CURRENT FILING DATE: 1999-10-08
                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acid
                               TYPE: PRT
ORGANISM: Ashbya gossypii
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930331
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Pred. No. 1.7e-09;
1; Mismatches 72;
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6291660mal Growth

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CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 878
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-934A-2
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US-09-735-934A-2
; Sequence 2, Application US/09735934A
; Patent No. 6372468
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APPLICANT: LI, Jiayin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEITILE OF INVENTION: THEREOF
FILE REFERENCE: CL000851
                                                                                                                                                                                                                                                                                                                                    Query Match 4.0%; Score 128.5; DB 4; Best Local Similarity 23.0%; Pred. No. 0.0048; Matches 88; Conservative 35; Mismatches 121;
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Best Local Similarity
Matches 83; Conserv
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                        231 PRRPP--
                                                      191 VDGPPGPVKKTRSIGSAVDQGNESIVAKTTVTVPNDGGPIEAVSTIETVPYW
                                                                                                   187
                                                                                                                                     132 QPSSSNAGNKRLSTIDESGSILSDISFD-KTDESLDWDSSLVKTFKLKKREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            764 SPVNATNESGISRSLQSMNLQAQYNAV------FG---ADLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     708 PTRPNDPNPVSLTSEEEK----EVKRRMKSFFPFKKLATTPTPYAAGNDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 VTVPNDGGPIEAVSTIETVPYWTRSRRKTGTLQPW------NSDS
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                                                                                                                                                                                                                                                       107 QLVRSSGDIQEGDLVEVVLSASATFEDF----QIRPHALTVHS------
                                                                                                                                                                                                                                                                               14 QLVRRVEILSEGNEVQFIQLAK-DFEDERKKWQRTDHELGKYKDLLMKAETE
                                                                                                                                                                                                                73 KHARNQVDVEIKRRQRAEADCEKL-ERQIQLIREMLMCDTSGSIQLSEEQKS
                                                                                                                                                                            -----YRAPAFCDHCGEMLFGLVRQGLKCDGCG---LNYHKRC
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                                                                                                   --NCSGARKRRLS----STSLASGHSVRLGTSESLPCTA----
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                      ---SSSSSSSSSSYT----GRPIEL---
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Pred. No. 5.1e-06;
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US-07-906-349A-5
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TITLE OF
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Browdy and Neimark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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FILING DATE: 18-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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381 TGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICSLLKDFLRNLKEPLLTFRLNR : |:| :| :| |:| :: :
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RANOVEL EXESSION-CLONING METHOD FOR
INVENTION: A NOVEL EXESSION-CLONING METHOD FOR
INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
INVENTION: TARGET PROTEINS
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                                                                                                                                                                                                                                                                          724 amino acids
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ilarity 22.2%;
Conservative 5
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                                                                                                                                                                                                                           linear
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                      Score 126.5; DB
Pred. No. 0.0054;
50; Mismatches 10
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US-08-167-035-2
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Best Local S
Matches 50
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 16-DEC-1993
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10036-2711
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                   AKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWSQ 541
                                                                                     AFME-AAEITDEDNSIAAMYQAV--GELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANL 496
                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                    EMISLAPEVQSSEEYIQLLKKLIRSPSIPHQYWLTLQYLLKHFFKLSQTSSKNLLNARVL
                                                                                                                        STLYRTQS-SSNLAELRQ-LLDCDTPSVDLEMIDVHVLADAFKRYLLDLPNPVIPAAVYS
                                                                                                                                                                                       PKPRPPRPLPVAPGSSKTEADVEQQALTLPDLAEQFAPPDIAPPLLIKLVEAIEKKGLEC
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MATGOLIS, Benjamin L.
VENTION: NOVEL EXPRESSION CLONING METHOD FOR VENTION: IDENTIFYING TARGET PROTEINS FOR EUKIVENTION: KTNASES AND NOVEL TARGET PROTEINS
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0; Mismatches 10
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RESULT 14
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US-08-208-887A-2
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                   Sequence 2, Application US/08539005 Patent No. 5858686
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   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COTUZZÍ, LBUTB A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 766
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                              Match 3.9%;
Local Similarity 22.2%;
les 50; Conservative 5
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     SEIFSPMLFRFSAASSD-----NTENLIKVIEILISTE---WNE 300
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                                                                                   Sequence 5, Appli
Patent No. 639158
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Best Local Similarity
                                                                     GENERAL INFORMATION:
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TELEX: 66141 PE
INFORMATION FOR SEQ
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NAME: Coruzzi, Laura A.
   APPLICANT:
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                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/
FILING DATE: 4-OCT-1995
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SOFTWARE: PatentI
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COTUZZI, LAUTA A.
COTUZZI, LAUTA A.
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                                                                                                 Application US/09280598
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            Schlessinger, Joseph
Skolnik, Edward Y.
Margolis, Benjamin L
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App, Harold
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Pred. No. 0.0054;
0; Mismatches 106;
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Gaps

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204

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TELEPHONE: (212) 790-9090

TELEPAX: (212) 899-9741/886:
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-280-598-5
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Search completed: July 3, 2003, 09:56:51 Job time: 31 secs
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PRIOR APPLICATION NUMBER: U5/08/252,820
FILING DATE: 02-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZ1, LAUIA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOKET NUMBER: 7683-067
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                             265 SEIFSPMLFRFSAASSD-----NTENLIKVIEILISTE---WNE 300
                                                                                                                                                                                                                             441 AFME-AAEITDEDNSIAAMYQAV--GELPQANRDTLAFLMIHLQRVAQ-SPHTKMDVANL 496
                                                                                                                                                                                                                                                                                                 147 STLYRTQS-SSNLAELRQ-LLDCDTPSVDLEMIDVHVLADAFKRYLLDLPNPVIPAAVYS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                           325 PECRDRCPLPCIPTLIGTPVKIGEGMLA--DFVSQTSP--MIPSIVVHCVNEIEQRGLTE 380
                                                                                                                                            497 AKVFGPTIVAHAVPNPDPVTMSQDIKRQPKVVERLLSLPLEYWSQ 541
                                                                                                                                                                                                205 EMISLAPEVQSSEEYIQLLKKLIRSPSIPHQYWLTLQYLLKHFFKLSQTSSKNLLNARVL 264
                                                                                                                                                                                                                                                                                                                             87 PKPRPPRPLPVAPGSSKTEADVEQQALTLPDLAEQFAPPDIAPPLLIKLVEAIEKKGLEC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A NOVEL EXPRESSION-CLONING METHOD FOR IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND NOVEL TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
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